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**FIGURE 178**

MPCAQRSWLANLSVVAQLLNFGALCYGRQPQPGPVRFPPDRRQEHFIKGLPEYHVVGPPVRVDAS  
GHFLSYGLHYPIITSSRRKRDLGSEDWVYYRISHEEKDLFFNLTVNQGFLSNSYIMEKRYGNL  
SHVKMMASSAPLCHLSGTVLQQGTRVGTAAALSACHGLTGFFQLPHGDDFFIEPVKKHPLVEGGY  
HPHIVYRRQKVPETKEPTCGLKGIVTHMSSWVEESVLFFW

**Signal peptide:**

amino acids 1-27

**N-glycosylation sites.**

amino acids 11-15, 105-109, 125-129

**N-myristoylation site.**

amino acids 149-155

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**FIGURE 179**

CAGATTTAAAAAGAAAACCTTTACTGAATCAGCTGAGTGTTAATAATACGAATTTCTTTTCT  
TGCCAATTCTGATCTGAACAGAAAATCCAAGAACAGGGAT**A**GTGTGGATTACAGTTTTCTCT  
GCCTTGCTACGACTGTTTTCTGGTGTTACCTGTTATCTTTTATTATTACTCCACAAAGAAAT  
ACTTGGATGTTCTGCTGTTTGTGCTGCTGCTGCTGGGAGACAAATTAAGTCCGCTAACTTAGG  
CCTTTCGAGTATTCCTAAGAATTTTCTGAAAGTACAGTTTTTCTGTAATCTGACTGGGAATAA  
TATATCTTATATAAAATGAAAGTGAATTAACAGGACTTCATTCTCTGTAGCATTGTATTGGGA  
TAATTTCTAACATTCTGTATGTATATCCAAAAGCCTTTGTTCAATTGAGGCATCTATATTTTCT  
ATTTCTAAATAATAATTTTCATCAAACGCTTAGATCCTGGAATATTTAAGGGACTTTTAAATCT  
TCGTAATTTATATTTACAGTATAATCAGGTATCTTTTGTTCGAGAGGAGTATTTAATGATCT  
AGTTTCAGTTTCAGTACTTAATCTACAAAGGAATCGCTCACTGTCTCTGGGAGTGGTACCTT  
TGTTGGTATGGTGCCTCTCGGATACTTGATTATCAAAACATAACATTTTGAGGATATCAGA  
ATCAGGCTTTCACACATCTTGAAAACCTTGCTTGTTGTATTAGGAAGTAATAATTTAACAAA  
AGTACCATCAATGCCTTTGAAGTACTTAAAGTCTTAGAAGACTTTCTTTGTCTCATAATCC  
TATTGAAGCAATACAGCCCTTTGCATTTAAAGGACTTGCCAATCTGGAATACCTCCTCTGAA  
AAATTCAGAATTAGGAATGTTACTAGGGATGGGTTTAGTGAATTAATAATCTTAAACATTT  
GATCTTAAGTCATAATGATTAGAGAATTTAAATTTTGACACATTCAGTTTGTTAAAGAATTT  
AATTTACCTTAAGTTAGATAGAAACAGAATAATTAGCATTGATAATGATACATTTGAAAATAT  
GGGAGCATCTTTGAAGATCCTTAATCTGTCAATTTAATAATCTTACAGCCTTGATCCAGGGT  
CCTTAAGCCGTTGTCTTCATTGATTCATCTTCAGGCAAAATCTAATCCTTGGGAATGTAACCTG  
CAAACTTTTGGGCTTCGAGACTGGCTAGCATCTTCAGCCATTACTCTAAACATCTATTGTCA  
GAATCCCCCATCCATGCGTGGCAGAGCATTACGTTATATTAAACATTACAATTTGTGTACATC  
TTCAATAAATGTATCCAGAGCTTGGGCTGTTGTAAAATCTCCTCATATTCATCACAAGACTAC  
TGCCTAATGATGGCTGGCATAAAGTAACCAAAATGGCAGTCTCTGGAAAATACTGAGAC  
TGAGAACATTACTTTCTGGGAACGAATTCCTACTTCACCTGCTGGTAGATTTTTTCAAGAGAA  
TGCTTTTGGTAATCCATTAGAGACTACAGCAGTGTTACCTGTGCAAAATACAACATTTACTATCT  
TGTTACCTTGAAGTTGGAAAAAACAGTGCTCTACCGAATGATGCTGCTCAATGTAGGGAA  
AACATCTCTAATTTGTACACAAGAAGTTGAGAAGTTGAATGAGGCTTTTGACATTTTGCTAGC  
TTTTTTCATCTTAGCTGTGTTTTAATCATTTTTTTGATCTACAAAGTTGTTTCAATTAACA  
AAACTAAAGGCATCAGAAAATCAAGGAAAATAGACTTGAATACTACAGCTTTTATCAGTC  
AGCAAGGTATAATGTAACTGCCTCAATTTGTAAACACTTCCCCAAATCTCTAGAAAAGTCCCTGG  
CTTGAGCAGATTGACTTCATAAAACAAATTTGTTCTGAAAATGAGGCACAGGTCATTCTTTT  
TGACATCTGCTTT**TAACT**CAACTAAATATTGTCTATAAGAACTTCAGTGCCATGGACAT  
GATTTAAACTGAAACCTCCTTATATAATTATATACTTTAGTTGGAATATAATGAATTATATG  
AGGTTAGCATTTATAAAATATGTTTTTNTTAAAAA

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**FIGURE 180**

MCGLQFSLPCLRLFLVVTCTYLLLLLHKEILGCSSVCQLCTGRQINCRNLGLSSIPKNFPFESTV  
FLYLTGNNISYINESELTGLHSLVALYLDNSNILYVYPKAFVQLRHLYFLFLNNFIKRLDPG  
IFKGLLNLRNLYLQYNQVSFVPRGVFNDLVSQYLNLRNRLTVLGSCTFVGMVALRILDLSN  
NNILRISESQFOHLENLACLYLGSNNLTKVPSNAFEVLKSLRRLSLSHNPIEAIQPPAFKGLA  
NLEYLLLLKNSRIRNVTRDGFSGINNKLHLILSHNDLENLNSDTFSLKKNLIYKLDRNRIISI  
DNDTFENMGASLKILNLSFNNTALHPRVLKPLSSLIHLQANSNPWECNCKLLGLRDWLASSA  
ITLNIYQNPSPMRGRALRYINITNCVTSSINVSRAWVVKSPHIIHKTTALMMAWHKVTTNG  
SPLENTETENITFWERIPTSPAGRFFQENAFGNPLETTAVLPVQIQLTTSVTLNLEKNSALPN  
DAASMSGKTSLICTEQVEKLENAFDILLAFFILACVLIIFLIYKVVOFKQKLKASENSRENRL  
EYYSFYQSARYNVTASICNTSPNSLESPLGLEQIRLHKQIVPENEAQVILFEHSAL

**Signal peptide:**

amino acids 1-41

**Transmembrane domain:**

amino acids 530-547

**N-glycosylation sites.**amino acids 71-75, 76-80, 215-219, 266-270, 317-321, 331-335,  
336-340, 400-404, 410-414, 451-455, 579-583**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 231-235

**N-myristoylation sites.**

amino acids 3-9, 69-75, 126-132, 174-180

**ATP/GTP-binding site motif A (P-loop).**

amino acids 506-514

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**FIGURE 181**

GGCCTGGCGCGCGCTCCGGTAAGGCGTGTGTGCGGCAGGGCGGGGACAGAACCGTCTCTCG  
GGCTCTGGGCGTGTCCGAGACCGCGCTCCCCGCCGAAATCAAGCTCCGAGTCATCCGTGTGGG  
GCATTCTGCCCCCTGGCACAGTTGGCCTCTTTCCAGAAGCCCGTTTTGTTTGTTTTACGCTCT  
AAATTGCGGTCGGTTCTTATTTCTCTCCCTGGCAAGGTCTGAAGACGGGTAGGAGAATAACCT  
GTGTGACGCGTGTATGATGCCGTCCCGTACCAACCTGGCTACTGGAATCCCCAGTAGTAAAGT  
GAAATATTCAAGGCTCTCCAGCACAGACGATGGCTACATTGACCTTCAGTTTAAGAAAACCCC  
TCCTAAGATCCCTTATAAGGCCATCGCACTTGCCACTGTGCTGTTTTGATTGGCGCCTTTCT  
CATTATTATAGGCTCCCTCCTGCTGTGACGGCTACATCAGCAAAGGGGGGCGAGACCGGGCCGT  
TCCAGTGCTGATCATTTGGCATTCTGGTGTCTACCCGATTTTACCACCTGCGCATCGCTTA  
CTATGCATCCAAAGGCTACCGTGGTTACTCCTATGATGACATTCCAGACTTTGATGACTAGCA  
CCCACCCATAGCTGAGGAGGAGTCACAGTGGAAGTGTCCAGCTTTAAGATATCTAGCAGAA  
ACTATAGCTGAGGACTAAGGAATTCTGCAGCTTGCAGATGTTTAAGAAAATAATGGCCAGATT  
TTTTGGGTCCCTTCCCAAAGATGTTAAGTGAACCTACAGTTAGCTAATTAGGACAAGCTCTATT  
TTTCATCCCTGGGCCCTGACAAGTTTTTCCACAGGAATATGTATCATGGAAGAATAGAGGTTA  
TTCTGTAATGGAAGTGTGCTGCCACCACCCTCTGTAGAGCTGAGCATTTCTTTTAAATA  
GTCTTCATTGCCAATTTGTTCTTGTAGCAAATGGAACAATGGGTATGGCTAATTTCTTATTA  
TTAAGTAGTTTATTTTAAAAATATCTGAGTATATTATCCTGTACACTTATCCCTACCTTCATG  
TTCCAGTGGAAGACCTTAGTAAATCAAGATCAGTGAGTTCATCTGTAATATTTTTTTTACT  
TGCTTTCTTACTGACAGCAACCAGGAATTTTTTATCCTGCAGAGCAAGTTTTCAAATGTAA  
ATACTTCCTCTGTTTAAACAGTCCTTGGACCATTCTGATCCAGTTTACCAGTAGGTTGGACAGC  
ATATAATTTGCATCATTTTGTCCCTTGTAATCAAGATGTTCTGCAGATTATTCCTTTAACGG  
CCGACTTTTGGCTGTTTCCTAATGAAACATGTAGTGGTTATTATTTAGAGTTTATAGCCGTA  
TTGCTAGCACCTTGTAGTATGTCATCATTCTGCTCATGATTCCAAGGATCAGCCTGGATGCCT  
AGAGGACTAGATCACCTTAGTTTGATTCTATTTTTTAGCTTGCAAAAAGTGACTTATATTCCA  
AAGAAATTAATATGTTGAAATCCAAATCCTAGAAATAAATGAGTTNNTTCCAAAAA  
AAA

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**FIGURE 182**

MMPSRTNLATGIPSSKVKYSRLSSTDG YIDLQFKKTPPKIPYKAIALATVLF LIGAFLLIIIG  
SLLLSGYISKGGADRAVPVLIIGILVFLPGFYHLRIAYYASKGYRGYSYDDIPDFDD

**Transmembrane domains:**

amino acids 45-66, 79-95

**N-myristoylation sites.**

amino acids 11-17, 75-81

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**FIGURE 183**

CTAAAAAATACAAAAATTAGCTGGCGCTGGTGTATGTACCTGTAATCCAGCTACTCAAGAGGCTGAGGCAGGA  
 GAATCGCTTGAACCCAGGAGGCGAGAGTTGCACTGAGCCAAGATTAACTGCTGAGCTCCAGGCTGGGTGACAGA  
 GCAAGACTCTGTATCAAAAATAAATAAAGTACAACCTCGGATGGGCTATGTGCTTATGTCTGTAATCCAG  
 CACTTTGGGAACCTTGAGGCGGGTAGATTGCTTGAGTCGGGAGTTTGAGACCAGCTCTGGTAAATATGGTAACCT  
 ATCAGCACTTCATTCCCTTCTATGGCTGAATAATAGTCCACTGTAGGGATGTGCCATGTTTTCCACTAGCTGAT  
 GGCATTTGGGTTGTTTTCCACCTCTCGCTATTATAAATATTGCTGCTATAAATATTCACCTACAAAGTTTTGTG  
 TGGACATATGTTTTATTTCTTCTGGTATATCCTTCGGAGTGGAACTGCTGGATCAGGTGGTAACTCTAGGTCTA  
 ACCTGGCAGTTAAACAGAATCCTATGCATGCTGTAGTCCATGAGTTGAAATAACACCTTGACCCATAGTAAGTGC  
 CAGATCATCTTCATTTACAGCAACCGTAATTTACAGATGAGGAAATGAAGGCTCCAGAGGTGAACCTGGCTT  
 TTCCCATTTGAGCAGTTCCAGTGCAGCAGTTAAAAAGTGGCAGGACCTGGAAAGAGAGCTAGTTCTTCCACCT  
 GGCATTACGGGCTGCCCTCGCGCTACGGGCTGGCATTAGAATAGAGCTAAGGTCTGTGCCAAAGCCAGGTGC  
 CCCAGTCTGCCCTCTCTGTCTTATTCACCTTTCTCTGCAGCCCTCCAGGGGACCCCTCTCTCAGGCCACCTC  
 TCTCTGGTGAAGTGCACAGTGTGCGGGAAGATCAAGATACGGTGCAGAACTGGCTTCGGACCATAGGACATT  
 CACAGCAGTGTATCCCGAGTGGGCAAGCCATTGACAGGAACCTCGACTCTGGAGATCTGTGGTGTGTGTCAGAT  
 GCGGTGTGGGACGCGGGGAGCAGCAGCAGCAGATCTTGCAGATGGCCATCGTGGAAACCTGTATCAGCAGGGC  
 ATGCTCAGCGTGGCCGAGGAGCTGTGCCAGGAATCAACGCTGAATGTGGACTTGGATTCAAGCAGCCTTTCCCTA  
 GAGTTGAATCGAATCCTGGAAGCCCTGCACGAACAGACCTGGGTCTCGCTTGGAATGGGCGCTCTCCACAGG  
 CAGCGCTGCTGGAACCTCAACAGCTCCCTGGAGTTCAAGCTGACCCGACTGCACTTCATCCGCTCTTGGCAGGA  
 GCGCCCGCGAAGCAGCTGGAGGCCCTCAGCTATGCTCGGCACCTTCCAGCCCTTTGCTCGGCTGCACCAGCGGGAG  
 ATCCGCTGATGTGGCAGCTGGTGTACCTGCGGCTGGAGAACTCAACCTACTGCCACCTGTCTGGAC  
 AGCAGCCACTGGGACAGATCTGTGAGACCTTTACCCGGGACGCTGTCCCTGCTGGGCTTCTGTGGAGTCC  
 CCCCCTAGCGTCAAGCTTTGCCCTGTGGCTGTGGCGCTGCCCTGTGTGATGAACATAAGGCTGTGATTGACACG  
 CGGCAGTGCATGGGCTTGGAAATCAAGAGGACGAGTTACCGATTGAGATTGAATAGGCATGAAGTCTGGTAC  
 GCTCATCTGTGGCCATGTTATCTCCCGAGATGCACTCAATAGCTCATTAATGGAGGAAACACTCCGCTGTTCCGT  
 TGCCCCATCTCCGCGAGCAGACGTGAGATCCAACCTCCCATCAAGCTGAAGTGTCCCTACTGTCCCATTGGAG  
 CAGAAGCCGCGAGATGGGAAACGATCATATTCGATTTCCTACCTGGAAAGGAATTTGCTGGAAGGGGTTTTAC  
 CTGTAGGCTTGGTCTGTCTCGGTAGGTTGGTCAACTTCAGTGGACTGTGGTTGGTTTCAGAGCGGCTGGCTGAG  
 GAGTTCCACTGAGGGGAGCACTGGAGCAGCCCTTTGGCAGAGGCTGAGGAGGAGATGGACAGGCCACGCTGG  
 CACCTGGCTCCTATGGCATAAGCAAGGGAGATGCTGGCCTCTGTGCTCTGTCTTTTCTTCTTCTGTTTCTG  
 GTTGACTTAGTAGAACCGACAAGATGGCAAGGGATTGGTCTTCAAGCAGTAGACATCCCTCCACCCCTGCCCT  
 CAGCCAGTCTCTTCTGCCATGCCAATGCTATGTCCACCTTGCCCTCGCCGCAAGAGTGTCCAGGGTGGCC  
 CACCTCTTCTCCCACTACAGCCTCAACAGTATGTACCATCTCCACTGTAATAGTCCCAGTTAGAACGGAATG  
 CGGTGTTTATAACTTTGAACAAATGATTTACTGCCCTTCTCAAAA

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**FIGURE 184**

QCCRKIKDTVQKLASDHKDIHSSVSRVGKAIDRNFSEICGVVSDAVWDAREQQQQIILQMAIV  
EHLYQQGMLSVAEELCQESTLNVLDLDFKQPFLELNRIEALHEQDLGPALEWAVSHRQRLEL  
NSSLEFKLHRLHFIRLLAGGPAKQLEALSARHFQPFARLHQREIQVMMGSLVYLRGLGKSP  
YCHLLDSSHWAIEICETFTTRDACSLLGLSVESPLSVSFASGCVALPVLMMNIKAVIEQRQCTGVW  
NHKDELPIEIELGMKCWYHSVFACPILRQQTSDSNPPIKLCGHVISRDALNKLINGGKLKCP  
YCPMEQNFPADGKRIIF

**Transmembrane domain:**

amino acids 222-241

**N-glycosylation site.**

amino acids 129-133

**Tyrosine kinase phosphorylation site.**

amino acids 151-159, 184-193

**Amidation site.**

amino acids 327-331

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 222-233

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**FIGURE 185**

GAGCGACGCTGTCTCTAGTCGCTGATCCCAAAATGCACCGGCTCATCTTTGTCTACACTCTAAT  
CTGCGCAAACCTTTTGCAGCTGTGCGGACACTTCTGCAACCCCGCAGAGCGCATCCATCAAAGC  
TTTGCGCAACGCCAACCTCAGGCGAGATGACTTGTACCGAAGAGATGAGACCATCCAGGTGAA  
AGGAAACGGCTACGTGCAGAGTCCTAGATTCCCGAACAGCTACCCAGGAACCTGCTCCTGAC  
ATGGCGGCTTCACTCTCAGGAGAATACACGGATACAGCTAGTGTTTGACAATCAGTTTGGATT  
AGAGGAAGCAGAAAATGATATCTGTAGGTATGATTTTGTGGAAGTTGAAGATATATCCGAAAC  
CAGTACCATTATTAGAGGACGATGGTGTGGACACAAGGAAGTTCTCCAAAGGATAAAATCAAG  
AACGAACCAAATTAATAATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAA  
GATTIATTATTCTTTGCTGGAAGATTTCCAACCCGCAGCAGCTTCAGAGACCAACTGGGAATC  
TGTCACAAGCTCTATTTAGGGGTATCCTATAACTCTCCATCAGTAACGGATCCCACTCTGAT  
TGCGGATGCTCTGGACAAAAAAATTGCAGAATTTGATACAGTGGAAGATCTGCTCAAGTACTT  
CAATCCAGAGTCATGGCAAGAAGATCTTGAGAATATGTATCTGGACACCCCTCGGTATCGAGG  
CAGGTCAACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCG  
TTACAGTTGCACTCCCAGGAATTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGGCCAATGT  
GGTCTTCTTTCCAGTTGCCTCCTCGTGCAGCGCTGTGGAGGAAATTGTGGCTGTGGAACTGT  
CAACTGGAGGTCTGCACATGCAATTGAGGAAAACCGTGAAGAAAGTATCATGAGGTATTACA  
GTTTGAGCCTGGCCACATCAAGAGGAGGGGTAGAGCTAAGACCATGGCTCTAGTTGACATCCA  
GTTGGATCACCATGAACGATGCGATTGTATCTGCAGCTCAAGACCACCTCGATAAGAGAATGT  
GCACATCCTTACATTAAGCCTGAGAGAA



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**FIGURE 186**

MHRLIFVYTLICANFCSCRDTSATPQSASIKALRNANLRRDDLYRRDETIQVKNGYVQSPRF  
PNSYPRNLLLTWRLHSQENTRIQLVFDNQFGLLEEAENDICRYDFVEVEDISETSTIIRGWCG  
HKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSLLEDFQPAAASETNWESVTSSISGVSY  
NSPSVTDPTLIADALDKKIAEFDTVEDLLKYFPESWQEDLENMYLDTPRYRGRSYHDKRSKV  
DLDRLNDDAKRYSCTPRNYSVNIREELKLANVVFPRCLLVQRCGGNCGCGTVNWRSCTCNSG  
KTVKKYHEVLQFEPGHIKRRGRAKTMALVDIQLDHHERCDCICSSRPFR

**Signal peptide:**

amino acids 1-18

**N-glycosylation site.**

amino acids 270-274

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 262-266

**Tyrosine kinase phosphorylation site.**

amino acids 256-265

**N-myristoylation sites.**

amino acids 94-100, 186-192, 297-303, 298-304

**TonB-dependent receptor proteins signature 1.**

amino acids 1-56

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**FIGURE 187**

CATGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGCGCGGCCCTTGGGGACGGGCAGTTCCCTG  
TGTCCTCTGGTGGTTTGCCTAAACCTGCAACATCACCTTCTTATCCATCAACATGAAGAATGT  
CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTT  
CATATATGGGCAAAAGAAATGGCTGAATAAATCAGAATGCAGAAATATCAATAGAACCTACTG  
TGATCTTTCTGCTGAAACTTCTGACTACGAACACCAGTATTATGCCAAGGTTAAGGCCATTTG  
GGGAACAAAGTGTTCCAAATGGGCTGAAAGTGGACGGTTCTATCCTTTTTTAGAAACACAAAT  
TGGCCCAACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTGTCTGACAGCTCC  
AGAGAAGTGGAAGAGAAATCCAGAAGACCTTCTGTTTCCATGCAACAAATATACTCCAATCT  
GAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAA  
CCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCCCTT  
CGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGA  
TCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTGCCATATCTATTACCGT  
GTTTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCAGTTGGCAAAGAGAAACA  
CCCAGCAAATTTGATTTTGTATTTATGGAATGAATTTGACAAAAGATTCTTTGTGCTGCTGA  
AAAAATCGTGATTAACCTTTATCACCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGA  
TATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAA  
CCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGA  
AATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCTCTCACCCAGCAAGAGTCCCTCAG  
CAGAACAATACCCCCGATAAAACAGTCATTGAATATGAATATGATGTCAGAACCACTGACAT  
TTGTGCGGGGCTGAAGAGCAGGAGCTCAGTTTGCAGGAGGAGGTGCCACACAAGGAACATT  
ATTGAGTGCAGGCAGCGTTGGCAGTCTTGGGCCCGCAAACGTTACAGTACTCATACCCCC  
TCAGCTCCAAGACTTAGACCCCCCTGGCGCAGGAGCACACAGACTCGGAGGAGGGGCCGGAGGA  
AGAGCCATCGACGACCTGGTCGACTGGGATCCCCAACTGGCAGGCTGTGTATTCTTCGCT  
GTCCAGCTTCGACCAGGATTCAGAGGGTGCAGCCTTCTGAGGGGATGGGCTCGGAGAGGA  
GGGTCTTCTATCTAGACTCTATGAGGAGCCGGCTCCAGACAGGCCACCAGGAGAAAATGAAAC  
CTATCTCATGCAATTCATGGAGGAATGGGGTTATATGTGCAGATGGAACTGATGCCAAACA  
CTTCCTTTTGCTTTTGTTCCTGTGCAAACAAGTGAGTCACCCCTTTGATCCCAGCCATAAA  
GTACCTGGGATGAAAGAAGTTTTTCCAGTTTGTGTCAGTGTCTGTGAGAA

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**FIGURE 188**

MPLPPLLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPEGLQGKVTYTVQYF  
IYGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTCKSKWAESGRFYPFLETQI  
GPPEVALTTDEKSIISVLTAFKWKRNPEDLPVSMQQIYSLKYNVSVLNTKSNRTWSQCVTN  
HTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLKDQSSEFKAKIIFWYVLPISITV  
FLFSVMGYSIYRIYHVGKEKHANLILYIGNEFDKRFFVPAEKIVINFITLNISSDDSKISHQD  
MSLLGKSSDVSSLNDPQPSPGNLRPPQEEEEVKHLGYASHLMEIFCDSEENTEGTSLTQQESLS  
RTIPDPKTVIEYEDVRTTIDICAGPEEQELSLQEEVSTQGTLLSQAAALAVLGPQTLQYSYTP  
QLQDLDPPLAQEHTDSEEGPEEPESTTLVDWDPQTGRLCIPSLSSFDQDSEGCEPSEGDLGEE  
GLLSRLYEPPAPDRPPGENETYLMQFMEEWGLYVQMEN

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 240-260

**N-glycosylation sites.**amino acids 31-34, 72-75, 80-83, 171-174, 180-183, 189-192,  
304-307, 523-526**Tyrosine kinase phosphorylation site.**

amino acids 385-392, 518-526

**N-myristoylation sites.**

amino acids 53-58, 106-111, 368-373, 492-497

**Tissue factor**

amino acids 1-278

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**FIGURE 189**

ATGTGCTGCTGGCCGCTGCTCTGCTGTGGGGGCTGCTCCCCGGGACGGCGCGGGGGGCTCG  
GGCCGAACCTATCCGCACCGGACCTCTCTGGACTCGGAGGGCAAGTACTGGCTGGGCTTGGAGC  
CAGCGGGGCAGCCAGATCGCCTTCCGCCCTCAGGTGCGCACTGCAAGGCTACGTTGGGCTTCCGG  
TTCTCGCCCAACGGGGCCATGGCGTCCGCCGACATCGTCTGGGGCGGGGTGGCCACGGGGCGG  
CCCTACCTCCAGGATTATTTTACAAATGCAAAATAGAGAGTTGAAAAAGATGCTCAGCAAGAT  
TACCATCTAGAAATATGCCATGGAAAATAGCACACACAATAATTGAATTTACCAGAGAGCTG  
CATACATGTGACATAAATGACAAGAGTATAACGGATAGCACTGTGAGAGTGATCTGGGCTTAC  
CACCATGAAGATGCAGGAGAAGCTGGTCCCAAGTACCATGACTCCAATAGGGGACCAAGAGT  
TTGCGGTTATTGAATCCTGAGAAAACCTAGTGTGCTATCTACAGCCTTACCATACTTTTGATCTG  
GTAAATCAGGACGTCCCCATCCCAAACAAAGATACAACATATTGGTGCCAAATGTTTAAAGATT  
CCTGTGTTCCAAGAAAAGCATCATGTAATAAAGGTTGAGCCAGTGATACAGAGAGGCCATGAG  
AGTCTGGTGACACCATCTGCTCTATCAGTGCAGCAACAACCTTAAACGACAGCGTTCTGGAG  
TCCGGCCACGAGTGCTATCACCCCAACATGCCCGATGCATTCCCTACCTGTGAAACTGTGATT  
TTTGCTGGGCTATTGGTGGAGAGGGCTTTTCTTATCCACCTCATGTTGGATTATCCCTTGGC  
ACTCCATTAGATCCGCATTATGTGCTCCTAGAGTCCATTATGATAATCCCCTTATGAGGAA  
AGTGGAAATTCATGTGTTTGCTGTTCTTCTCCATGCTCACCCTGGCTGGCAGAGGCATCAGGCTG  
GGGGTGATTGAGGCTGGCCTCTGGGTGAGCCTCTTCCATACCATCCCTCCAGGGATGCCTGAG  
TTCAGTCTGAGGGTCACTGCACCTTTGGAGTGCCTGGAAGAGGCTCTGGAAGCCGAAAAGCCA  
AGTGGAAATTCATGTGTTTGCTGTTCTTCTCCATGCTCACCCTGGCTGGCAGAGGCATCAGGCTG  
CGTCATTTTCGAAAAGGGAAGGAAATGAAATTACTTGCCATGATGATGATTTTGACTTCAAT  
TTCAGGAGTTTCAGTATCTAAAGGAAGAACAACAATCTTACCAGGAGATAACCTAATTACT  
GAGTGTGCTACAAACAGAAAGATAGAGCTGAGATGACTTGGGGAGGACTAAGCACCAGGAGT  
GAAATGTGCTCTCATACCTTCTTTATTACCCAAGAATTAATCTTACTCGATGTGCAAGTATT  
CCAGACATTATGGAACAACCTTCAGTTCATTGGGGTTAAGGAGATCTACAGACCAGTCACGACC  
TGGCCTTTTCATTATCAAAAGTCCCAAGCAATATAAAAACCTTTCTTTCATGGATGCTATGAAT  
AAGTTTAAATGGACTAAAAAGGAAGGTCTCTCCTTCAACAAGCTGGTCTCAGCCTGCCAGTG  
AATGTGAGATGTTCCAAGACAGACAATGCTGAGTGGTCGATTCAAGGAATGACAGCATTACCT  
CCAGATATAGAAAGACCTTATAAAGCAGAACCCTTGGTGTGTGGCAGCTCTTCTTCTCTCC  
CTGCACAGAGATTTCTCCATCAACTTGCTTGTTGCTTCTGCTACTCAGCTGCACGCTGAGC  
ACCAAGAGCTTGTGA~~TC~~CAAAATTTCTGTTGGACTTGACAATGTTTCTATGATCTGAACCTGTC  
ATTTGAAGTACAGGTTAAAGACTGTGTCCACTTTGGGCATGAAGAGTGTGAAGACTTTTCTTC  
CCATTTTCCCTCCCTTCCTTTTCTTTCCATGTTACATGAGAGACATCAATCAGGTTCTCTT  
CTCTTTCTTAGAAATACCTGATGTTATATATACATGGTCAATAAAATAAACTGGCCTGACTT  
AAGATAACCATTTTAAAAAATTGGGCTGTCATGTGGGAATAAAGAAATCTTTCTTTCTCTAA  
AAAAAAA

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**FIGURE 190**

MCCWPLLLLWGLLPGTAAGSGRTPHRTLDDSEGKYWLGWSQRGSQIAFRLQVRTAGYVGFG  
FSPTGAMASADIVVGGVAHGRPYLQDYFTNANRELKKDAQQDYHLEYAMENSTHTIIIEFTREL  
HTCDINDKSITDSTVRVIWAYHHEDAGEAGPKYHDSNRGTSLSRLNPEKTSVLSTALPYFDL  
VNQDVPIPNKDTTYWCQMFKIPVFQEKHHVIKVEPVIQRGHESLVHHILLYQCSNNFNDSVLE  
SGHECYHPNMPDAFLTCETVIFAWAIGGEGFSYPHVGLSLGTPLDPHYVLLEVHYDNPTYEE  
GLIDNSGLRLFYTMDIRKYDAGVIEAGLWVSLFHTIPPGMPEFQSEGHCTLECLEEAELEAEKP  
SGIHVFAVLLHAHLAAGRIRLRHFRKGKEMKLLAYDDDFDNFQEFQYLKEEQTILPGDNLIT  
ECRYNTKDRAEMTWGGLSTRSEMCLSYLLYPRLNTRCASIPDIMEQLQFIGVKEIYREVTT  
WPFIIKSPKQYKNLSFMDAMNKFVKWKKEGLSFNKLVLSPVNVRCSTDNAEWSIQGMTALP  
PDIERPYKAEPLVCGTSSSSSLHRDFSINLLVCLLLLSCTLSTKSL

**Signal peptide:**

amino acids 1-18

**Transmembrane domains:**

amino acids 56-73, 378-393, 583-602

**N-glycosylation sites.**

amino acids 114-118, 247-251, 476-480, 517-521

**N-myristoylation sites.**amino acids 11-17, 15-21, 20-26, 45-51, 68-74, 79-85, 290-296,  
316-322, 337-343, 342-348, 456-462, 534-540, 582-588**Copper type II, ascorbate-dependent monooxygenases proteins.**

amino acids 271-321, 422-474

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**FIGURE 191**

GCTTCAGCTGAAGAAAGAGAGGAAATGAAGCGCCTTCTGCTTCTGTTTTGTTCTTTATAACAT  
TTTCTTCTGCATTTCCCTTAGTCCGGATGACGGAATGAAGAAAATATGCAACTGGCTCAGG  
CATATCTCAACCAGTTCTACTCTCTTGAAATAGAAGGGAATCATCTTGTTCAAAGCAAGAATA  
GGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCATTTTTTGGATTGACAGTGACTGGAA  
AACTGGACTCAAACACCCTTGAGATCATGAAGACACCCAGGTGTGGGGTGCCTGATGTGGGCC  
AGTATGGCTACACCTCCCTGGGTGGAGAAAATACAACCTCACCTACAGAATAATAAACTATA  
CTCCGGATATGGCACGAGCTGCTGTGGATGAGGCTATCCAAGAAGGTTTAGAAGTGTGGAGCA  
AAGTCACTCCACTAAAATTACCAAGATTTCAAAGGGGATTGCAGACATCATGATTGCCTTTA  
GGACTCGAGTCCATGGTCCGTGTCCTCGCTATTTTGATGGTCCCTTGGGAGTGCTTGGCCATG  
CCTTTCCTCCTGGTCCGGGTCTGGGTGGTGACACTCATTTTGATGAGGATGAAAACCTGGACCA  
AGGATGGAGCAGGATTCACCTTGTTTCTGTGGCTGCTCATGAATTTGGTCATGCACTGGGGC  
TCTCTCACTCCAATGATCAAACAGCCTTGATGTTCCCAAATTATGTCTCCCTGGATCCCAGAA  
AATACCCACTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTATGGAGGTCTGCCTAAGG  
TACCTGCTAAGCCAAAAGGAACCCACTATACCCCATGCCTGTGACCTGACTTGACTTTTGACG  
CTATCACAACTTCCGCAGAGAAGTAATGTTCTTTAAAGGCAGGCACCTATGGAGGATCTATT  
ATGATATCACGGATGTTGAGTTTGAATTAATTGCTTCATTTCTGGCCATCTCTGCCAGCTGATC  
TGCAAGCTGCATACGAGAACCCAGAGATAAGATTCTGGTTTTTAAAGATGAAAACCTTCTGGA  
TGATCAGAGGATATGCTGTCTTGCCAGATTATCCCAAATCCATCCATACATTAGGTTTTCCAG  
GACGTGTGAAGAAAATAGATGCAGCCGTCTGTGATAAGACCACAAGAAAAACCTACTTCTTTG  
TGGGCATTGTTGCTGGAGGTTTGATGAAATGACCCAAACCATGGACAAAGGATTCCCGCAGA  
GAGTGGTAAACACTTTCTGGAATCAGTATCCGTGTTGATGCTGCTTTCCAGTACAAAGGAT  
TCTTCTTTTTCAGCCGTGGATCAAAGCAATTTGAATACAACATTAAGACAAAGAATATTACCC  
GAATCATGAGAACTAATACTTGGTTTCAATGCAAAGAACCAAAGAACTCCTCATTTGGTTTTG  
ATATCAACAAGGAAAAAGCACATTCAGGAGGCATAAAGATATTGTATCATAAGAGTTTAAGCT  
TGTTTATTTTTGGTATTGTTTCATTTGCTGAAAAACACTTCTATTATCAATAAATTCATAGAC  
CTAAAATAAACCTCAACAGGTCTTTTAATATAAATTCTGCTTCAAATAGAATAAAACCATTC  
TTTAACAAC

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**FIGURE 192**

MKRLLLLLFLFFITFSSAFPLVRMTENEENMQLAQAYLNQFYSLIEIGNHLVQSKNRSLIDDKI  
REMQAFFGLTVTGKLDSENTLEIMKTPRCGVDPVGQYGYTLPGWRKYNLTYYRIINYTPDMARAA  
VDEAIQEGLEVWSKVTPLKFTKISKGIADIMIAFRTRVHGRCPRYFDGPLGLVGHAFPPGPGL  
GGDTHFDEDENWTKDGAGFNLFLVAAHEFGHALGLSHSNDQTALMFFPNYVSLDPRKYPLSQDD  
INGIQSIYGGPLKVPKPKPEPTIPHACDPDLTFDAITTFRREVMMFFKGRHLWRIYYDITDVEF  
ELIASFWPSLPADLQAAYENPRDKILVFKDENFWMIRGYAVLPDYPKSIHTLGFPGRVKKIDA  
AVCDKTRTKTYFFVGIWCWRFDEMTQTMKGFPQRVVKHFPGISIRVDAAFQYKGGFFFSRGS  
KQFEYNIKTKNITRIMRTNTWFOCKEPPKNSSFGFDINKEKAHSGGIKILYHKSLSLFIFGIVH  
LLKNTSIYQ

**Signal peptide:**

amino acids 1-17

**N-glycosylation sites.**

amino acids 55-59, 110-114, 200-204, 452-456, 470-474, 508-512

**N-myristoylation site.**

amino acids 71-77, 205-211, 223-229

**Hemopexin domain signature.**

amino acids 171-202, 207-238, 318-334

**Neutral zinc metalloproteinases, zinc-binding region signature.**

amino acids 213-223

**Matrixins cysteine switch.**

amino acids 89-97, 207-238

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**FIGURE 193**

CACAATCAGGTCCCATTTCTATAGATGGGGAAACTGAGGCTTGAGGTCACATAGGCGTCGTTCA  
AGGCTGGTATACCTGCACCCTCTCCCATGTGAACAACATGGTTCGGGTAATGGGGGCTGTCA  
TCCAGTCTCCTCCCTGCCCCCTGCTGGTGCACCTTCCTGCCTCTGCTGGTGCACTTTCTGCCCCT  
ACTGGTATATTTGCTGCCTCTGCTGGGGCGCTTCCTGCCTCGGCTGGTGTATCTCCTGCCCCT  
GCTGGTGCACTTTCTGCCCCGCTGATGCACCTTCCTGCCTCTGCTGGTGCACCTTCCTGGCTCT  
GCTGGCACACTTCCTGCCTCTGCTGGTGCACCTTCCTGGCTCTGCTGGCGCACTTCCTGCCCC  
TGCTGGTGTATTTCTGCCCCCTGCTGGTGTACTTCCTTCCCCTGCTGGTGCACCTTCCTGCCTC  
TGCTGGCGCACTTCCTGCCTCTCCAGGCCCTACCTTAGCCCTCTCCCTCTTATATATGGAAGTCT  
TCCAGTTCACCTGACACTGGTAACAGGGACTCTGCTCTTGGTGTGCTGTCTGCCCCGGGGAT  
GGGCATCTGTGTCTTCTTTACTACTGCTGGCTCAGGACCCAGAGCTTTGAAGCATGTCCAGA  
TGCAGGTCCGGGCACCAGAGTCTAAGGAGCCCCTACACCCACCAGGATTTTCCAATAAAGAGA  
TGTTACCA



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**FIGURE 194**

MVLGNGGCHPVSSLP LLVHFLPLL VHFLPLL VYLLPLLGRFLPRLVYLLPLL VHFLPPLMHFL  
PLL VHFLALLAHFLPLL VHFLALLAHFPAPAGVFPAPAGVLPSPAGALPASAGALLASPGPT

**Signal peptide:**

amino acids 1-39

**N-myristoylation sites.**

amino acids 4-10, 109-115, 116-122

**Leucine zipper pattern.**

amino acids 14-36, 16-38, 17-39, 21-43, 24-46, 28-50, 31-53,  
35-57, 38-60, 42-64, 45-67, 49-71, 52-74, 56-78, 59-81, 63-85,  
65-87, 66-88



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**FIGURE 196**

MRRLTRRLVLPVFGVLWITVLLFFWVTKRKLEVPTGPEVQTPKPSDADWDDLWDQFDERRYLN  
AKKWRVGGDDPYKLYAFNQRESERISSNRAIPDTRHLRCTLVYCTDLPPTSIIITFHNEARST  
LLRTIRSVLNRTPTHIREIILVDDFSNDPDDCKQLIKLPKVKCLRNNERQGLVRSRIRGADI  
AQGTTLTFLDSHCEVNRDWLQPLLHRVKEDYTRVVCVIDIINLDTFTYIESASELRGGFDWS  
LHFQWEQLSPEQKARRLDPTFPIRTPIIAGGLFVIDKAWFDYLGKYDMMDIWGGENFEISFR  
VVMCGGSLEIVPCSRVGHVFRKKHPYVFPDGNANTYIKNTKRTAEVWMDEYKQYYYAARPFAL  
ERFFGNVESRLDLRKNLRCQSFKWYLENIPELSIPKESSIQKGNIRQRQKCLESQRQNNQET  
PNLKLSPCAKVKGEDAKSQVWAFTYTQQILQEELCLSVITLFPGAPVVLVLCKNGDDRQQWTK  
TGSHEHIAHLCLDTDMFGDGTENGKEIVVNPCESSLMSQHWDMVSS

**Transmembrane domain:**

amino acids 475-493

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 2-6

**Tyrosine kinase phosphorylation sites.**

amino acids 68-75, 401-409

**N-myristoylation sites.**

amino acids 178-184, 186-192, 192-198, 346-352, 383-389, 526-532

FIGURE 197

[illegible]

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**FIGURE 198**

MGEDDAALRAGSRGLSDPWADSVGVRPRTERHIAVHKRLVLAFAVSLVALLAVTMLAVLLSL  
RFDECCGASATPGADGGPSGFPERGGNGSLPGSARRNHAGGDSWQFEAGGVASPGTTSAQPPS  
EEEREPEWEPWTQLRLSGHLKPLHYNMLTAFMENFTFSGEVNVIEACRNATRYVVLHASRVAV  
EKVQLAEDRAFGAVPVAGFFLYPQTQVLVVVLNRTLDAQRNYNLKI IYNALIENELLGFFRSS  
YVLHGERRFLGVTQFSPTHARKAFPCFDEPIYKATFKISIKHQATYLSLSNMPVETSVFEEDG  
WVTDHFSQTPLMSTYYLAWAICNFTYRETTTKSGVVRLYARPDARRGSGDYALHITKRLE  
FYEDYFKVPYSLEPKDLLAVPKHPYAAMENWGLSIFVEQRILLDPSVSSISYLLDVTMVIVHE  
ICHQWFGDLVTPVWWEDVWLKEGFAHYFEFVGTDYLYPGWNMEKQRFLLDVLHEVMLLDGLAS  
SHPVSQEVLQATDIDRVFDWIAYKKGAALIRMLANFMGHSVFQRLQDYLTIHKYGNAARNOL  
WNTLSEALKRNGKYVNIQEVMDQWTLQMGYPVITILGNTTAENRIITQQHFIYDISAKTKAL  
KLQNNSYLWQIPLTIIVVGNRSHVSSEAIWVSNKSEHHRITYLDKGSWLLGNINQTCYFRVNY  
DLNRWRLIIDQLIRNHEVLSVSNRAGLIDDAFSLARAGYLPQNIPILEIIRYLSEEKDFLPWA  
ASRALYPLDKLLDRMENYNIFNEYILKQVATTYIKLGWPKNNFNGSLVQASYQHEELRREVIM  
LACSGFNKHCHQQAASLTISDWISSNRNRIPLNVRDIVYCTGVSLDEDEVFEIWMKFHSTTAV  
SEKKILLEALTCSDDRNLLNRLNLSLNSEVLDQDAIDVIIHVARNPGRDLAWKFFRDKWK  
ILNTRYGEALFMYSKLISGVTEFLNTEGELKELKNFMKNYDGVAAASFRAVETVEANVRWKM  
LYQDELFWQLGKALRH

**Transmembrane domain:**

amino acids 44-63

**N-glycosylation sites.**amino acids 89-93, 160-164, 175-179, 222-226, 338-342, 605-609,  
634-638, 649-653, 663-667, 684-688, 800-804, 906-910**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 362-366

**Tyrosine kinase phosphorylation site.**

amino acids 520-528

**N-myristoylation sites.**amino acids 78-84, 87-93, 90-96, 118-124, 501-507, 604-610,  
825-831, 987-993**Neutral zinc metalloproteinases, zinc-binding region signature.**

amino acids 437-447

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**FIGURE 199**

GCGCCCGGCGCAGCTCGGCCAGAGCGACCGCGGGGCTGAGCGCGCTCCGCCAGGGGGCTCCGGAAGCTGCCCC  
 GGCCCGGGGCTCTCTCCCTCGCTCCCGCTTCCCGCTTCTCGCTCAGCGCGCGCTCCCTTCCCGAGCTCCCTCGCC  
 GTCCCGCCCGCCACAGCCAGGCGCTCCGCGCCCTCGACGCCACGATCGCCCGGGCCCGCCCGCCCGCGCGGG  
 ACTCGCCGGGATCTCGCTGTTCCCTCGCTCTGCTCTCGGGAGCCCGGCGGACGCTGGAGCGAGTGTCTCTTCC  
 CGAGGGAGATGCTAGCCCTTTGGTGCTTCTTACCTCTCGCTCAGGAGCCCGGAGAGGAGCTCTCTGCACAAAG  
 GCACCCCTGAAGAGAGAGTGGTAAACAGCGCCCGCCAGTTCTCTCACAGTCGSGCGGAAGTGTCTGGCGAGCTGTGTCT  
 GGATGGGACCGACCCCTCTGCACATACAGACATCCACAGCCCTGTACCGCTGCTTCCAGAGGAGSGCCCGCCCAA  
 GCACGGCTTGCCCCCAAGAGAGAACTGCGCTTCGCTCAAGCAGGTGAACCTTCGCCAGGAAGCAGTGCAGGCCCAA  
 GGCCACCTTCGCGAGCCACTGTCCAAAGGGCAGGGTCCAGCCAGCGTCCAGGGGCTAGATCTCTCTCTCTCTCT  
 CACGGAGAAGCCTGGCCCAACCGGGGACCCGGACCCCATCTGTGGCTCCGAGGAGGATCAGAAGTGCCCTTTG  
 GCTGGATCGAAAGGAGAGTGCGGTCCTTACAACACCCGACCCCTGCAAACTCTCCCCCTTCACTTCGCGAGCCCTA  
 TGTGGCCACACACTCCCCAGAGGCCAGAAACCGGGGAGCTGGGCTGACATGGCCAGGAGGCCCGCCAGGA  
 GGACACCGAGCCCATGGCCCTGATGGACAAAGTGAGAATGAGCTGACTGGGTGAGCCCTCAGAGGAGAGCCAGGA  
 GACCACTACCTCCACATTATCACCAACACGGTCTATCACACCGAGCAAGCAGCTCTCTCGAGTGTGAGCTT  
 CTCGAATCCTGAGGGTACATTGACTCCAGCGACTACCCACTGCTGCCCTCAACAACCTTTCTGGAGTGACATTA  
 CAACGTGACAGTCTACACTGGCTATGGGTGGAGCTCCAGGTGAAGAGTGAACCTCTCCGATGGGGAACGTCT  
 CTCCTATCGCGGGGTGGAGGGCCCTACCTTGACCTCTGCGCCACACAGCAAGCTCCTGGTGGAGGGGCGAGTAA  
 CCGAGGCCCAACCAACCACTCTCCGCTACTTCCGGACCTTCAGGACGAGCGGCTTGGGACCTTCCAGCTTCA  
 TTACAGGCCCTTCACTGCTGAGCTGCAACTTCCCGCGCGCTGACTCTGGGAGTGTCAGGTTGAGCTTGCAT  
 CTCAGGTGGGTGCCCACTTCACTGCCACCTGGGCTATGAGCTCCAGGGCGCTAAGATGCTGACATGCATCAA  
 TGCTCCAAAGCGGCACTGGAGCAGCCAGGAGCCCATCTGCTCAGCTCCTTTGGAGGGGCACTGCACAATGCCAC  
 CATCGGCGCGCTCTCTCCCCAAGTTACCTGAAAAACAAATGGGAGCCAACTTCTGCACTCTGGACGATTGAAGC  
 TCCAGAGGGCCAGAACTGCACCTTGACCTTTGAGAGGCTGTTGCTGCATGACAAGGACAGGATGACGGTTACAG  
 CGGGCAGACCAACAGTCACTTCTCTACGACTCCCTTCAAACCGAGAGTGTCCCTTTTGGAGGCGCTGCTGAG  
 CGAAGCAACCACTCCGATCGAGTTCAGCTCCGACAGGCCGGGCGGCTTCAACATCCGATTTGA  
 AGCTTTGAGAAAGCCACTGCTATGAGCCCTACATCCAGAAATGGGAACCTCACTACATCCGACCCGAGCTATAA  
 CATTTGGGACTATAGTGGAGTCACTTCGCGACCCCGGCCACTCCCTGGAGCAGGCGCGGCCATCACTCGAATGCAT  
 CAATGTGCGGGACCCATCTGGAATGACACAGAGCCCTGTGACAGGCATGTGTGTGGGAGCTCTCTGCTGT  
 GGCTGGGGTGGTATTGTCCCCAACTGGCCGAGCCCTACGTGGAGGTTGAAGATTGTATCTGGAAGATCCAGT  
 GGGAGAAGAGAAACGGAATCTTCTAGATATCCAGTTCTGAACTGAGCAACAGTGACATCTTGACCATCTACGA  
 TGGCGACGAGGTGATGCCCACTCTTTGGGGCAGTACCTTGGGAACAGTGGCCCCAGAACTGTACTCTCCAC  
 GCCAGACTTAACCATCCAGTTCCATTTCGACCCCTGCTGGCTCATCTTTGGAAGGGGCGAGGATTTATCATGAA  
 CTACATAGAGGTATCAGGAATGACTCCTGCTCGGATTTACCCGAGATCCAGAAATGGCTGGAAACCACTTCTCA  
 CACGGAGTTGTTGCGGGGAGCCAGAATCACTTACAGTGTGACCCGGCTATGACATCTGGGGGATGACACCT  
 CAGCTGGCAGTGGGACCTCAGCTGGAGCAGGACCCCACTTTTGTGAGAAATATGATGCTGCACCGACCCCGG  
 AGAGCTGAGCTGCTGACCCGCTTAATTTCCGATCTGTGCTGCTGGGAGCAACCACTCAATCAACCTCGAA  
 CCCCCTTTTGTGCTTGAAGGAGTCTCTCTTCTGACCTGTCTACAGCCGTGAACACAGGAGCTCCCATCTGGAGCT  
 TCGCTGCCCACTGCTTTTCGAGGAGTCCCTGGCATGTGACAACCCAGGCGCTGCCATAAATGGATACCAAT  
 CTGTACAGGAGCATCTACTGCGCAGGAGAGTCCCTTCATGTGCTAGAAAGCTTTGAGCTCATGGGTGA  
 AGTGACCATCCGCTGCATCTCTGGACAGCCATCCCACTGGAGACGGGCGCTGCCGTGTGAAAGTTAATCAAGA  
 CAGTTTGAACATGCTTTAGAAGCAGAAGCGGACGACAGACGTCGCTGGAGGGGGGAGCATGGGCCCTGGCTAT  
 CTTCTCCGGTCTCATCATCTCTTACTGCTGGGAGGAGCCACTATTACATCACAAAGATGTGCTACTATTTC  
 CAACTCTCGCCCTGCTCTGATGACTCTCCACCTACAGCCAGATCACCTGGAAACCGAGTTTGACACCCCAAT  
 TTACGAGCAGGGGAAACAGAGAGTATGAGGTTTCTATCTAAAGAGAGCTACACTTCCAGAGGGGACTTTGGA  
 CTCACCCACAATCTCTCCGAGACTTATCCAGAGACCATGTGGCACTTGATTGAACCCCAAGATGTGCACTGT  
 CTTTTGTCTAGACTCTTTATCAAGGTTTACTGTTTCTTCCCTGATTTATTATATTTAAAGTGAAAAA  
 AAAAAA

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**FIGURE 200**

MPAARPPAAGLRGISLFLALLLGGSPAAALERDALPEGDASPLGPYLLPSGAPERGSPPGKEHPE  
 ERVVTAPPSSSSQSAEVLGELVLVDGTAFSAHHDIPALSPDLLPEEARPKHALPPKKKLPSPKQVN  
 SARKQLRPKATSAATVQRAGSQFPASQGLDLLSSSTEKPGPPGDPDPFIVASEEASEVPLWLDRK  
 ESAVPTTFAPLQISPTTSQPYVAHTLPQRPEPEGEPGPDMAQEAPQEDTSPMALMDKGENELTG  
 SASSEESQETTTSTIITTTVITTEQAPALCSVSFSNPEGYIDSSDYPLLPLNNELECTYNVTVY  
 TGYGVELQVKSNNLSDGELLSSIRGVDGPTLTVLANQTLLVEGQVIRSPNTNTISVYFRTFQDDG  
 LGTFQLHYQAFMLSCNFFRRPDSGDVTVMDLHSGGVAHFHCHLGYELQGAKMLTCINASKPHW  
 SSQEPICSAAPCGGAVHNATIGRVLSPSYPENTNGSQFCIWTIEAPEGQKLHLHFERLLHDKD  
 RMTVHSGQTNKSALLYDSLQTESVPFEGLLSEGNTIRIEFTSDQARAASFNIRFEAFKKGHC  
 YEPYIQNGNFTTSDPTYNIGTIVEFTCDPGHSLEQGPAAIECINVRDPYWNDEPLCRAMCGG  
 ELSAVAGVVLSPNWPEPYVEGEDCIWKIHVGEEKRIFLDIQFLNLSNSDILTIYDGEVMPHI  
 LGQYLGNSGPPQKLYSSPTDLTIQFHSDPAGLIFGKGQGFIMNYIEVSRNDSCLDLPEIQNGWK  
 TTSHTELVRGARITYQCDPGYDIVGSDTLTCQWDLSSWSDPPFCEKIMYCTDPGEVDHSTRLI  
 SDPVLVGTTIQYTCNPGFVLEGSSLLTCYSRETGTPIWTSRLPHCVSEESLACDNPGLPENG  
 YQILYKRLYLPGESLTFMCYEGFELMGVEVTRCILGQPSHWNGPLPVCKVNQDSFEHALEAEA  
 AAETSLEGGNMALAFIPVLIISLLGGAYIYITRCRYYSNLRPLMYSHPYSQITVETEFDN-  
 PIYETGETREYEVSI

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 893-915

**N-glycosylation sites.**

amino acids 311-315, 328-332, 350-354, 435-439, 458-462, 474-478,  
 514-518, 576-580, 618-622, 674-678, 742-746

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 188-192

**N-myristoylation sites.**

amino acids 23-29, 87-93, 146-152, 454-460, 475-481, 575-581,  
 629-635, 695-701, 723-729, 766-772, 877-883, 953-959

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 383-394

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**FIGURE 201**

GATGGCTACGGCAGGGGGTGGCTCTGGGGCTGACCCGGGAAGTCGGGGTCTCCTTCGCCCTTCT  
GTCTTTCTGCGTCTTACTAGCAGGTTTGTGCAGGGGAACTCAGTGGAGAGGAAGATATATAT  
CCCCTTAAATAAAACAGCTCCCTGTGTCGCCCTGCTCAACGCCACTCATCAGATTGGCTGCCA  
GTCTTCAATTAGTGGAGACACAGGGGTTATCCACGTAGTAGAGAAAGAGGAGGACCTACAGTGT  
GGTATTGACTGATGGCCCCAACCCCCCTTACATGGTTCTGCTGGAGAGCAAGCATTTTACCAG  
GGATTTAATGGAGAAGCTGAAAGGGAGAACAGCCGAATTGCTGGTCTTGCAGTGTCTTGCAC  
CAAGCCAGTCTCTGCCCTCAGGCTTCTCTCTAGTGTACAGTGGCCCAATGTATGGGTTTGGTGT  
TTACTCCAATTCTATGGGGCAGAGTTTGCTCACTGCAGAGAAATACAGTGGAAATTCGCTGGG  
CAATGGTTTGGCTTATGAAGACTTTAGTTTCCCCATCTTTCTTCTTGAAGATGAAAAATGAAC  
CAAAGTCATCAGCAGTGTCTATCAAGATCACAACTGAGTCAGAATGGCTCAGCACCAACCTT  
CCCCTATGTGCCATGCAGTCTTTTACACATGTCATGCTGTATCAGCACTGCCACCTGCAT  
GGCGCGCAGCTCCATCCAAAGCACCTTCAGCATCAACCCAGAAATCGTCTGTGACCCCTGTCT  
TGATTACAATGTGTGGAGCATGCTAAAGCCTATAAATACAACCTGGGACATTAAAGCCTGACGA  
CAGGGTTGTGGTTGTGTCACCCCGGCTGGATAGTCGTTCTTTTCTGGAATGTGGCCCCAGG  
GGCTGAAGCGCAGTGGCTTCTTTGTCAACCAGCTGGCTGCTGTGAAGCTTTGCAAAAGGC  
ACCTGTATGACACCTGCCCGCCCAATGTCTGTTTCTCTTCTTCAAGGGGAACTTTTGA  
CTACATTGGCAGCTCAGGATGGTCTACGATATGGAGAAGGGCAAGTTTCCCGTGCAGTTAGA  
GAATGTGACTCATTTGTGGAGCTGGGACAGGTGGCCTTAAGAACTTCATTAGAGCTTTGGAT  
GCACAGCATCTGTTTCTCAGAAAAATGAGTCTGTACGGAAACAGGTGGAGGATCTCTGGC  
CACATTGGAGAAGAGTGGTCTGCTGCTGCTGTATCTCAGGAGGCCAAATCAGTCCCA  
GCCCTCCCACTCTTCTCTGCAGCGATTTCTTCAGCTCGAAACATCTCTGGCGTTGTTCT  
GGCTGACCATCTGGTGGCTTCCATAACAAAATATTACCAGAGTATTACGACACTGCTGAGAA  
CATTAATGTAGCTATCCCGAATGGCTGAGCCCTGAAGAGGACCTGAACTTTGTAAACAGACAC  
TGCCCAAGGCCCTGGCAGATGTGGCCACGGTGTGGGACGTGCTGTATGAGCTTGCAGGAGG  
AACCACCTTCAGCGACACAGTTTACGGCTGATCCCCAAACGGTTACCCGCTGCTCTATGGGTT  
CCTGATTAAAGCCAACTCATGGTTCCAGTCTATCTCAGGACAGGACCTAAGGTCCTACTTT  
GGGTGACGGGCTCTTCAACATTACATCGCTGTCTCCAGCCCCAACACCACTTATGTGTGT  
ACAGTATGCTTGGCAAATTTGACTGGCACAGTGGTCAACCTCACCCGAGAGCAGTGCCAGGA  
TCCAAGTAAAGTCCCAAGTGAAGAAACAGGATCTGTATGAGTACTCATGGGTCCAGGGCCCTTT  
GCATTTAATGAGACGGACGACACTCCCCGGTGTGTGCGTTCTACTGCAGCATAGCCAGGGC  
CTTGCTCTCTGCCCTTTGAAGTGTGCTGAGTGGAGCTCTACTGAATACTCTACATGGAGTGTGAG  
CCGCTGGAAGATATCCGTGCCCGGATATTTCTCATGCGCAGCAAGAGCTTGAATGTATCAC  
CCTGACATCTGGGCTTCGGCTCCTCATCTTCTCCCTCATCGTCACTGTCATGCAATGCCAAC  
AGCTGATGTCTTTTTCATTGCTCCCGGGAGCCAGGAGCTGTGTATACATGAGGAGGACCCCA  
GCTTTTCTTGCAGNTCAGCAGTTCACTTCCTAGAGCATCTGTCCCACTGGGACACAACTCACT  
AATTTGTCACTGGAACTCCCTGGGCTGTCTCAGATTGGGATTACATATAAGAGAGTGGAACT  
ATCCAAAAGAGACAGGAGAGAAATAAATAAATAGCCTCCCTTCTCCGCTCCCTTTCCCATCA  
CCCCCTCCCCATTTCCCTCTTCTCTACTCATGCCAGATTTTGGGATTACAATAGAAGCT  
TCTGTGCTCTGTTTAACTCCTAGTTACCCACCTAATTTGCCCTTCAGGACCTTCTACTTT  
TTCTTCTCTGCCCTGTACCTCTCTCTGCTCCTCACCCCCACCCCTGTACCCAGCCACCTTCTCT  
GACTGGGGAAGGACATAAAAGGTTTAAATGTACAGGTCAAACATACATTGACCCCTGAGGCCAGG  
GGCATCTCTGGGCTGAGCTGTCTCTCTCCCACTGTCTCTTCTCCAGGCCCTCAGATGGC  
ACATTAGGGTGGGCGTGTGCGGGTGGGTATCCCACTCCAGGCCACAGTGTCTCAGTTGTACT  
TTTATTAAAGCTGTAATATCTATTTTGTGTTTTGTCTTTTCTTTTATCTTTTGTAAATAT  
ATATATAATGAGTTTCATTAAAAATAGATTATCCC



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**FIGURE 202**

MATAGGGSGADPGSRGLLRLLSFCVLLAGLCRGNSVERKIYIPLNKTAPCVRLLNATHQIGCQ  
SSISGDTGVIHVVEKEEDLQWVLTGDPNPPYMVLLSKHFTRDLMEKLGKRTSRIAGLAVSLT  
KPSPASGFSVSPVQCPNDGFGVYSNSYGPEFAHCREIQWNSLGNGLAYEDFSFPIFLLEDENET  
KVIKQCYQDHNLSQNGSAPTFFPLCAMQLFSHMHAVISTATCMRRSSIQTFSINPEIVCDPLS  
DYNVWSMLKPIINTTGTCLKPDDRVRVVAATRLDSRSFFWNVAPGAESAVASFVTQLAAAEALQKA  
PDVTTLPRNVMFVFFQGETFDYIGSSRMVYDMEKGKFPVQLENVDSFVELGQVALRTSLELWM  
HTDPVSQKNESVRNQVEDLLATLEKSGAGVPAVILRRPNQSQPLPPSSLQRFLRARNISGVVL  
ADHSGAFHNKYYQSIYDTAENINVSYPEWLSPEEDLNFVTD TAKALADVATVLGRALYELAGG  
TNFSDTVQADPQTVTRLLYGFLIKANNSWFQSILRQDLRSYLGDGPLQHYIAVSSPTNTTYVV  
QYALANLTGTVVNLTREQCQDPQSKVPSENKDYEYSWVGPLHSNETDRLPRCVRSTARLARA  
LSPAFELSQWSSTEYSTWTESRWKDIRARIFLIASKELELITLTVGFGILIFSLIVTYCINAK  
ADVLFIAPREPGAUSY

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 671-692

**N-glycosylation sites.**

amino acids 45-49, 55-59, 187-191, 200-204, 204-208, 264-268,  
387-391, 417-421, 435-439, 464-468, 506-510, 530-534, 562-566,  
573-577, 580-584, 612-616

**Glycosaminoglycan attachment site.**

amino acids 404-408

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 232-236

**N-myristoylation site.**

amino acids 5-11, 6-12, 9-15, 29-35, 61-67, 120-126, 146-152,  
168-174, 205-211, 294-300, 438-444, 446-452, 504-510, 576-582

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**FIGURE 203**

GCTAGACCGAGCCCTGGGAGGCTACGGGCTCCCCGGAAACCCCTGCCAGGGGAGCCGGGTTTT  
GAGCTCAGGCGCCTCTAGCGGGCGGCCCCAGAAATCTGACTCGCGAGGCCAGAGTTGCAGGGA  
CTGAATAGCAAACTGAGGCTGAGTAGGGAACAGACCATGAGGTCAGTGCAGATCTTCCTCTCC  
CAATGCCGTTTGGCTCCTTCTACTAGTTCCGACAATGCTCCTTAAGTCTCTTGGCGAAGATGTA  
ATTTTTACCCTGAAGGGGAGTTTGACTCGTATGAAGTCACCATTCCCTGAGAAGCTGAGCTTC  
CGGGGAGAGGTGCAGGGTGTGGTCAGTCCCGTGTCTACCTACTGCAAGTTAAAGGCAAGAAG  
CAGTCCCTCCATTTGTGGCCCAAGAGACTTCTGTTGCCCCGACATCTGGCGGTTTTCTCCTTC  
ACAGAACATGGGGAAGTCTGCTGGAGGATCATCCTTACATACCAAAGGACTGCAACTACATGGGC  
TCGTTGAAAGAGTCTCTGGACTCTAAAGCTACTATAAGCACATGCATGGGGGGTCTCCGAGGT  
GTATTTAACATTGATGCCAAACATTACCAAATTGAGCCCCCTCAAGGCCCTCTCCAGTTTTGAA  
CATGTCGTCTATCTCCTGAAGAAGAGCAGTTTGGGAATCAGGTTTGTGGCTTAAGTGATGAT  
GAAATAGAATGGCAGATGGCCCCCTTATGAGAATAAGGCGAGGCTAAGGGACTTTCCTGGATCC  
TATAAACACCCAAAGTACTTGGAAATTGATCCTACTCTTGTATCAAAGTAGGTATAGGTTTGTG  
AACAACAATCTTTCTCAAGTCATACATGATGCCATTCTTTTGACTGGGATTATGGACACCTAC  
TTTCAAGATGTTCGTATGAGGATACACTTAAAGGCTCTTGAAGTATGGACAGATTTTAACAAA  
ATACCGGTTTGATATCCAGAGTTAGCTGAAGTTTAGGCAAGTTGTAATATATAAAAAAGT  
GTATTAATGCTCGCCTGTATCAGATTGGGCACATTTATATCTTCAAAGAAAAATATAATGAT  
GCTCTTGCATGGTCGTTTGGAAAAGTGTGTTCTCTAGAATATGCTGGATCAGTGAGTACTTTA  
CTAGATACAAATATCCTTGCCCCCTGCTACCTGGTCTGCTCAGTCTGGGTCATGCTGTAGGA  
ATGTCACATGATGAACAATACTGCCAATGTAGGGGTAGGCTTAATTGCATCATGGGCTCAGGA  
CGCACTGGGTTTAGCAATTGCAGTTATATCTCTTTTTTAACATATCTCTTCGGGAGCAACA  
TGCTAAATAATATCCAGGACTAGGTTATGTGCTTAAGAGATGTGGAAAACAAATTTGTGGAG  
GACAATGAGGAATGTGACTGTGGTTCCACAGAGGAGTGTGAGAAAGATCGGTGTTGCCAATCA  
AATTGTAAGTTGCAACCAAGTGCCAACCTGTAGCATTGGACTTTGCTGTCTATGATTGTCCGTTT  
CGTCCATCTGGATACGTGTGTAGGCGAGGAAGGAAATGAATGTGACCTTGCAGAGTACTGCGAC  
GGGAATTCAGTTTCTGCCCCAATGACGTTTATAAGCAGGATGGAACCCCTTGAAGTATGAA  
GGCCGTTGTTTCAGGAAGGGTGCAGATCCAGATATATGCAGTGCCAAAGCATTTTTGGACCT  
GATGCCATGGAGGCTCCTAGTGAGTGCTATGATGCAGTTAACTTAATAGGTGATCAATTTGGT  
AAGTGTGAGATTACAGGAATTCGAAATTTAAAAAGTGTGAAAGTGCAAAATCAATATGTGGC  
AGGCTACAGGTGATAAATGTGAAACCATCCCTGATTTGCCAGAGCATACGATATAATTTCT  
ACTCATTTACAGGCAGAAAACTCATGTGCTGGGACACAGGCTATCATCTATCCATGAAACCC  
ATGGGAATACCTGACCTAGGTATGATAAATGATGGCACCTCCTGTGGAGAAGGCCGGGTATGT  
TTTAAAAAAATTTGCGTCAATAGCTCAGTCCGTCAGTTTGACTGTTTGCTGAGAAATGCAAT  
ACCCGGGGTGTTTGCAACAACAGAAAAAAGTCCCACTGCATGTATGGGTGGGCACCTCCATTC  
GTGAGGAAGTGGGGTATGGAGGAAGCATTGACAGTGGGCTCCAGGACTGCTCAGAGGGGCG  
ATTCCGTCGTCAATTTGGGTTGTGTCCATCATATAATGTTTCGCTTATTTTATTAATCCTTTCA  
GTGGTTTTGTGTTTTTCCGGCAAGTGATAGGAAACCACTTAAACCCAAACAGGAAAAATG  
CCCAATTCCAAAGCAAACTGAACAGGAAGAATCTAAACAAAAAAGTACAGGAAGAATCT  
AAACAAAAAAGTGGACAGGAAGAATCTGAAGCAAAAGTGGACAGGAAGAATCTAAAGCAAAA  
ACTGGACAGGAAGAATCTAAAGCAAACTTGAAGTAACGACCCAAAGCAAGAGTGTCAAG  
AAACAAAAAAGTAAACCGGCAATCCATACTCATTCAGTAACACAGGCTCATTATTTAAACCA  
GCTAATCATTTATCCAAAGGCTTCCATTCTTCCCAATATTTTTTTTACTTTAATTTTCCC  
ACAAGTTTTGATCAGCAATAAACAGCATTCTGTTTTGGAACAAAAA

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**FIGURE 204**

MRSVQIFLSQCRLLLLLVPTMLLKS LGEDVIFHPGEFEFDSYEVTIPEKLSFRGEVQGVVSPVS  
YLLQLKGKKHVLHLWPKRLLPRHLRVFSFTEHGELLEDDHPYIPKDCNYMGSVKESLDSKATI  
STCMGGLRGVFNIDAKHYQIEPLKASPSFEHVYLLKKEQFGNQVCGLSDDDEIEWQMAPYENK  
ARLRDFPGSYKHPKYLELILLFDQSRYSRVNNLSQVIHDAILLTGIMDTYFQDVRMRIHLKA  
LEVWTDENKIRVGPPELAEVLGRFVIYKKSVLNARLSSDWAHLYLQRKYNDA LAWSFGKVCSL  
EYAGSVSTLLDTNILAPATWSAHELGHAVGMSHDEQYCQCRGLNCIMGSGRTGFSNCSYISF  
FKHISSGATCLNNIPGLGYVLKRCGNKIVEDNEECDGSGTEECQKDRCCQSNCKLQPGANC SI  
GLCCHDCRFRPSGYVCRQEGNECDLAEYCDGNSSSCPNDVYKQDGTGPKYEGRCFRKGCRSRY  
MQCQSIFGPDAMEAPSECYDAVN LIGDQFGNCEITGIRNFKKCESANSICGRLQCIN VETIPD  
LPEHTTIIISTHLQAENLMCWGTGYHLSMKPMGIPDLGMINDGTSCGEGRVCFKKNCVNSSVLQ  
FDCLPEKCNTRGVCNNRNKNCCHMYGWAPPFCEEVGYGGSIDSGPPGLLRGAIPSSIWVVSIIIM  
FRLILLILSVVFVFRQVIGNHLKPKQEKMPLSKAKTEQEESKTKTVQEESKTKTGQEESEAK  
TGQEESKAKTGQEESKANIESKRPKAKSVKKQKK

**Signal peptide:**

amino acids 1-27

**Transmembrane domain:**

amino acids 684-705

**N-glycosylation sites.**

amino acids 222-226, 372-376, 438-442, 473-477, 625-629

**N-myristoylation sites.**amino acids 131-137, 168-174, 235-241, 319-325, 364-370, 436-442,  
472-478, 609-615, 642-648, 668-674, 676-680, 680-686, 749-755,  
758-764, 767-773**Amidation site.**

amino acids 69-73

**Disintegrins proteins**

amino acids 429-479

**EGF-like domain proteins**

amino acids 650-662

**Neutral zinc metalloproteinases, zinc-binding region proteins**

amino acids 335-345

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**FIGURE 205**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGGGAAGGTTGAATGGGGTAGAAGGCCTG  
TTGTGGAGGGAAACCCATCCTCCTGCTCCACCACCACCATCATCTGGCTGGACGGAG  
AGGGTGACGGGGGCTGGGAAGGGGCAGCTCATGTTCAAGGTTTCCAGGAGGGGCTACCTGTTGA  
CTGTCTTTTGCAGGAAGAAGAAAAACACCTGAGTGACCAGATGCCAGCTCCAGGTGCTTGGC  
AGATGGCCAGAACCACACCTCTTGAAGAGTGACAGTGCTGTGGAGCATGGTTTCTGACACCT  
GGAATGACTGGAACCCCAAGACTCAAGAAGGAGCTAAAGATCTTGAAGTAGACATGAATAAA  
ACAGAAGGCTGTGGAGCCACCTGTGCGAGATGGAGAAGTCCTTCTGAGGCTATCCAAACACGGC  
CAGGCCATGAGACCCCGATGACCATCCCTGAATTTTTTTCGAGAGTCAGTCAACCGATTGGAA  
CTTATCCAGCCCTCCCATCCAAGAATGGCAAAAAGTGGGAAATTTCTGAATTTCAACCAGTACT  
ATGAGGCTTGTGCGAAGGCTGCAAAATCCTTGATCAAGCTGGGTTTGGAGCGTTTCCACGGAG  
TTGTATCTCTGGGTTTAACTCTGCAGAGTGGTTATCACTGCTGTTGGTGCCATCTAGCCG  
GGGTCCTTGTGTTGGTATTTATGCCACCAACTCTGCCGAGGCTTGTCAATATGTCATCACTC  
ATGCCAAAAGTGAACATCTTGTCTGGTTGAGAATGATCAACAGTTACAGAAAAATCCTTTCGATTC  
CACAGAGCAGCTAGAGCCCTAAAAGGCATCATCCAGTACAGACTGCCAATGAAGAAGAACA  
ACAACCTGTACTCTTGGGATGATTTTCATGGAACCTTGGCAGAAGTATCCCTGACACCCAACTGG  
AGCAGGTCATCGAGAGCCCAAGGGCGAATCAATGGCAGTGCTCATCTACACTTCACAGGACCA  
CAGGCATACCAAGGGAGTGATGCTCAGTCATGACAACATCACGTGGATTGACAGGAGCAGTGA  
CAAAGGACTTTAACTGACAGACAAGCATGAGACGGTGGTTAGCTACCTCCCACTCAGCCATA  
TTGCGACGCAGATGATGGACATCTGGGTACCCATAAAGATTGGGGCGCTCACATACTTTGCTC  
AAGCAGATGCTCTCAAGGGGACCTTGGTAAGTACTCTAAAGGAGGTAAGAACCTACTGTCTTCA  
TTGGAGTGCCTCAAATTTGGGAGAAGATACATGAGATGGTGAAGAAAAATAGTGCCAAAGTCCA  
TGGGCTTGAAGAAGAAGGCATTCTGTGGGCAAGAAACATTGGCTTCAAGGTCACACTCAAAAA  
AGATGTTGGGGAATAATAATACTCCCGTAGCTACCGCATGGCTAAGATCTCTGTGTTACGCA  
AAGTCAAGACATCCCTTGGCTTGGATCACTGTCACTCTTTTATCAGTGGGACTGCGCCCTCA  
ACCAAGAGACTGCCGAGTTCTTTCTAAGCTTGGACATACCTATAGGCGAGTTGTATGGGTTGA  
GTGAGAGCTCGGGACCCACACGATATCCAACCAAGATAACTACAGGCTTCTAAGCTGTGGCA  
AGATCTTGACTGGGTGTAAGAATATGCTGTTCCAGCAGAACRAGAGTGGCATTGGGGAGATCT  
GCCTCTGGGGTAGGCATCTCATGGGCTATCTGGAAAGTGAGACTGAAACTACAGAGGCCA  
TCGATGATGAAGGCTGGCTCACTCTGGGGATCTGGGCCAGCTGGACGGTCTGGGTTTCTCTCT  
ATGTCACCGGCCACATCAAGAAATCCTTATCACTGCTGGTGGTGAATGTGCCCCCATTC  
CTGTTGAGACCTTGGTTAAGAAGAAGATCCCCATCATCAGTAACGCCATGTTAGTAGGAGATA  
AAGTGAAGTTTCTGACATGTTGCTGACGCTGAAGTGTGAGATGAATCAGATCAGCGGAGAAC  
CTCTGGAAGCTGAACCTCGAGGCCATCAACTTCTGTGCGGGCTTGGGCAGCCAGGCTTCCCA  
CCGTGACTGAGATTGTGAAGCAGCAAGACCCCTGGTCTACAAGGCCATCCAGCAAGGCATCA  
ATGCTGTGAACAGGGAAGCCATGAACAATGCACAGAGGATTGAAAAGTGGGTCTATCTGGAGA  
AGGACTTTTCCATCTATGGTGGAGAGCTAGGTCCAATGATGAAACTTAAGACATTTTGTATG  
CCAGAAATACAAAAACAAATTGATCACATGTACCCTGACTGCTTTGATGGAGCTGCTCTC  
AGCTGTTCTGATGCCCTTCAGCAGGAAGACCTCATTGCAATAAGTGAAATGCTGCTCAGGTAG  
AAGCTCTCCCTGCTGTTTTAAGAAGCCACATTCCTCATTGGTCAGTTTCTGTGATGTTGCTG  
TGTGGAGAGGTGCTCCCTAGAAGAACCTGCCATACGTTTCAAAGCAATAAAATCACTGTATA  
TCTTTCTAAGGACCTTCAAGTCATGACTCCAGGGAAGCCCTATTGGGAAGTCTACTAAAACTG  
CCTGATTTACAAGAAACACTGAACCTTGTGGGCTCCCAATTTGATTTTTTTCTCTCAGGGGAC  
TCAGACATTAAGAAGAAAAAGCCTCACAGATTTGAAGAAGTGGACCCCCAAATCAACTCACCT  
GCCTGGAAGCAACTGGGAAACCTTCCAATAACTCCTGATAATAAAGCACTTCAGGGTCCCAA  
AAAAAAAAA

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**FIGURE 206**

MTIPEFFRESVNRFGTYPALPSKNGKKWEILNFNQYYEACRKAASKSLIKLGLERFHVGVGILGF  
NSAEWFITAVGAILAGGLCVGIYATNSAEACQYVITHAKVNILLVENDQQQLQKILSIPQSSLE  
PLKAIQYRLPMKKNNNLYSWDDFMELGRSIPDTQLEQVIESQKANQCAVLIYTSGTTGIPKG  
VMLSHDNITWIAGAVTKDKFKLTDKHETVVSYLPLSHIAAQMMDIWVPIKIGALTYFAQADALK  
GTLVSTLKEVKPTVFIGVPIWEKIHVMVKNSAKSMGLKKKAFVWARNIGFKVNSKKMLGKY  
NTPVSYRMAKTLVFSKVKTSGLDHCFSFISGTAPLNQETAEFFLSLDIPIGELYGLSESSGP  
HTISNQNNYRLLSCGKILTCKNMLFQQNKDGIGEICLWGRHIFMGYLESETETTEAIDDEGW  
LHSGDLGQLDGLGFLYVTGHIKEILITAGGENVPPIPVETLVKKKIPPIISNAMLVGDKLKFLS  
MLLTLCCEMNQMSGEPDKLNFEAINFCRGLGSQASTVTEIVKQQDPLVYKAIQQGINAVNQE  
AMNNAQRIEKWVILEKDFSIIYGELGPMMLKRRHFVAQKYKQIDHMYH

**Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 65-86

**N-glycosylation site.**

amino acids 196-200

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 282-286

**Tyrosine kinase phosphorylation sites.**

amino acids 547-555, 608-616

**N-myristoylation sites.**amino acids 15-21, 74-80, 80-86, 84-90, 185-191, 189-195,  
253-259, 337-343, 371-377, 448-454, 536-542**Amidation site.**

amino acids 24-28

**Putative AMP-binding domain signature.**

amino acids 177-189

**Putative AMP-binding domain proteins.**

amino acids 173-190

FIGURE 207

[illegible]

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**FIGURE 208**

MAYRVLGRAGPPQPRRARRLLFAFTLSLSCTYLCYSFLCCDDLGSRLLGAPRCLRGPSAGG  
QKLLQKSRPCDPSGPTPSEPSAPSAPAAAVPAPRLSGSNHSGSPKLGTKRLPQALIVGVKKGG  
TRAVLEFIRVHPDVRLGTEPHFFDRNYGRGLDWYRSLMPRTLESQITLEKTPSYFVTQEAPR  
RIFNMSRDTKLIVVVRNPVTRAISDYTTLSKKPDIPTFEGLSFRNRTLGLVDVSWNAIRIGM  
YVLHLESWLQYFPLAQIHVFSGERLITDPAGEMGRVQDFLGIKRFITDKHIFYFNKTKGFPCLK  
KTESSLLPRCLGKSKGRTHVQIDPEVIDQLREFYRPNYIKFYETVGQDFRWE

**Signal peptide:**

amino acids 1-33

**N-glycosylation sites.**

amino acids 102-106, 193-197, 235-239, 306-310

**Tyrosine kinase phosphorylation site.**

amino acids 296-305

**N-myristoylation sites.**

amino acids 51-57, 100-106, 121-127, 125-131

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 20-31

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**FIGURE 209**

CTTTCCTTATCTGTGTGTACTCTTATCTCACTGTTCTATTTTTTCTCCTCATTATATTAAC  
 CTTTCTTACCTTTTTTCTGAACCTCTAGGCCCTTCTCTTCCAGAACTGGTGGGAAGCAAAATG  
 AAACGGCCAAGATGGTAAGAAACAAGCCGCATTTCTCCTTGGGGAGACTGATAATTTAAAGG  
 TTTGTTGTGTGCAGAAACATTTCCAGCTTCATCACCACCCCTTTCCTTCCACCTCTGCCCACTG  
 GAGACCATTACATCCGAAGCGGACGCGGCAGCTGAAGTCAGGAACCATGCATCACCATTAG  
 CAGGAGCCAACCTGCAGACTTTAAACTCCGTTCAACATGTGGATGCGGCAGAGAAATGACCTGT  
 CCAGACAAGCCGGGGCAGCTCATAAACTGGTTTCATCTGCTCCCTGTGCGTCCGCGGGGTGCGT  
 AAGCTCTGGAGCAGCCGGCTCCAAGGACCCGGAGAAACCTTCTGCTGGGCACCTGCGTGTGCC  
 ATCTACTTGGGCTTCTCTGGTGAGCCAGGTGGGGAGGGCCTCTCTCCAGCATGGACAGGCGGCT  
 GAGAAGGGGCCACATCGCAGCCGCGACCCGCGAGCCATCCTTCCCTGAGATACCCCTGGAT  
 GGTACCTTGGCCCTCCAGAGTCCAGGGCAATGGTCCACTCTGCAGCCCAATGTGGTGTAC  
 ATTACCTTACGCTCCAAGCGCAGCAAGCCGGCCAATATCCGTGGCACCCTGAAGCCCAAGCGC  
 AGGAAAAGCATGCACTGGCATCGGCTGCCCAGGGCAGGAGGCTTGGTCCGACCATCCCTT  
 CAGCCGCAAGGAAGCGCAAGGGAAGCTGATGCTGTAGCACCTGGGTACGCTCAGGGAGCAAA  
 CTGGTTAAGATTGGAGAGCAGCCCTGGAGGTTGGTGCGGGGTCCGGAGTGCGAGCCGGGGG  
 CAGACTTCTCAGCCGCTGAGGCTCCAGGGAGAGCAACATTAGGATCTCAGCGCAGGCGGCCCC  
 TCTTGGCTGAGCAAAAGATGCATCCGAAGAATGCGACTCTTGGCGGACAGCGCAGTGGCAGGG  
 CTCGGGCTGTGCTCTTAGGAGCGGAGCCCGTTTGTCTGGTGTGGAGGGGGGCGCACCTGGC  
 GCTGTGCTCCGCTGTGGCCCTAGCCCTGTGGGCTTCTCAAGCAGCCCTTGGACATGAGTAG  
 GTGTTTGCTTCCACCTAGACAGGATCTTGGGGCTCAACAGGACCTGCCGTCTGTGAGCAGG  
 AAAGCAGAGTTCATCAAGATGGCCGCCATGCCCATCATCTTTGGGATGCATCTTTATCT  
 TCAGAAAGATGACACCCATTCTTCTGTAAAGCTACCTGGGAACTTATCAGCATGTGCTG  
 AAACAGAAATGCTGGCAGATGGCCGAGTACCAAGCCTGAATCAGGTTGTACTGAAATACAT  
 CATCATGAGTGGTCCAAGATGGCAGCTCTTGATTTTTTGTACAGATTATAATCGTTAGAT  
 ACAAAATTGCTGTGGATTACAGCCTCGCAAGGAAGATGCCTGTGTACAGAAATGGATTGAGGCCA  
 AAATGTGATGACCAAGGTTCTGCGGCTCTAGCACACATTATCCAGCGAAAGCATGACCCAAGG  
 CATTGTTTTTATAGACAACAAGGTTCTTTGACAGGAGTGAAGATAACTTAAACTTCAAA  
 TTTGTAGAAGGCATCAAAAGATTTCCAGCTTCTGCAGTTTCTGTTTTGAAGAGCCAGCACTTA  
 CGGCAGAAACTTCTTCACTCTGTTTCTTGATAAAGTGATTGGGAAAGCTCAAGGAGGTAGA  
 CAAGGAATTGAAAGCTTATCGATGTAATAGAACACAGAGCAAAATTTCTTACCTATATATC  
 AATGCACACGGGGTCAAAGTATTACCTATGAATGAATGACAAAAGAATCTTCTGGCTAGGGTG  
 TTAGATATATTATGCATTTTGGTTTTGTTTTTAAATCAAGCACATCAACCTCAAGCCCGTT  
 TAGCAATGAGGCAGTGTAGATGAATACGTAAATAAATGACTTTAACCAGTACGCTATAAAGG  
 GACTTAGCACTGTATCACTACTTAAAAAGGTTTTGAAAAACAACTACTTGGAGAAATATTTGT  
 TTTATATTTTCTCTAACATGCTATGTGTGAGTCTGAACATCTGACAAACAGAAATTTTCAGT  
 TATTATTTCTAGCTAAGTTTGAAGAACATTGTGCATGCTGTTTAAAGAAACCTGCAAAACCGA  
 GATACTGACTCCATTAAATAACCATATTTTGTGCCGTTTTGACTGTTCTGACCAAAATACTAAT  
 GGGACAAATCTTGCAGTTTTCTGTTGCTGATTGTTAAATAGAGCAGTCTCTACACTACCC  
 TGAGGCAACTCTACATTTGGAACACTGAGGCTTACAGCCTGCAAGAGCATCAGAGCTGACCATA  
 CATTAAACAGAAATGCTGGTTTATTTGCAAAATCACCAGTATATTTTCTATTGTGTCTATAA  
 AAAATCAGTCATTTAAGTACAAGAAATCATATTTCCATTCTTTTGAAGAAATTTATTTTGTG  
 TCCCTATGGAATATTTACATCTGACAATTTATATGTAAAGAGTTTTTACTCTCTTATTTT  
 GGTCCAATTTGTATCTAGTGGCTGAGAAATTAATAAATCTAAAGTATGAAGTTACCTATCTG  
 AAAATGTACTTACAGAGTATCATTTTAAATGGATGTCCTTTTAAAAATTTTGTACTTTTAC  
 ACAAACTGTAATATAATTTATGTATATTTTATTAATAAGTGAATCTCTTAAATTTTGTCT  
 ATGTACTTATATTTAATTTGATTTAATGGTTTACTGCCAGATATTGAGAAATGGTTCAAATAT  
 TGAGTGTGTTTTCAATAA



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**FIGURE 210**

MTC PDKPGQLINWFICSLCVPRVRKLWSSRRPRTRRNLLLGTACAIYLGFLVSQVGRASLQHG  
QAAEKGP HRSRD TAEP SFPEI PLDGT LAPPESQNGSTLQPNVVYITLRSKR SKPANIRGTVK  
PKRRKKH AVASAA PGQEALVGP SLQPQEAA READAVAPGYAQGANLVKIGERP WRLVRGPGVR  
AGGPDFLQ PSSRESNIRIYSESAPS WLSKDDIRRMRL LADS AVAGLRPVSSRS GARLLVLEGG  
APGAVLR CGPSPCGLLKQPLDMSEVF AFHLDRI LGLNRTLPSVSRKAEFIQDGRFCPIILWDA  
SLSSASNDTHSSVKLTWGTYQQLLKQKCWQNGRVPKPESGCTEIH HHHEWSKMA LFD FLLQIYN  
RLDTNCCGFRPRKEDACVQNGLRPKCDDQGSAA LAHIIQRKHDPRHLVFIDNKGFFDRSEDNL  
NFKLLEGIKEFPASAVSVLKSQH L RQKLLQSLFLDKVYWESQGG RQGI EKLIDVIEHRAKILI  
TYINAHGVKVLPMNE

**Transmembrane domain:**

amino acids 40-56

**N-glycosylation sites.**

amino acids 98-102, 289-293, 322-326

**N-myristoylation sites.**amino acids 8-14, 41-47, 97-103, 187-193, 251-257, 252-258,  
287-293, 484-490

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**FIGURE 211**

TGGGGTGGTGAGCGCAGCGCCGAGG**ATG**AGGAGGTGCAACAGCGGCTCCGGCCCGCCGCGTGCCTGCTGCTGC  
 TGCTGCTCTGGCTGCTGCGGGGTTCGCCGGCTAACCGCGCCCCGGGTGCGGCGCTCTATTGCCCTTCCGACCCCG  
 TGACCGTCTGCGAGCGGACAGCGGTGCGCGCGCGGTGCTGGGCTCCCGCAGCGCTGGGCCCTGGGCTTGCATCTTCG  
 CCTCTGTGTGCGGCCATGCACTGGCTTCGCCCGCAGCTGGAAGGCGCTGGCCGAGAGCTCAAGAGCTGGAGGCG  
 CGGCTCTGTATCTCGCCGCCCTTGAAGTGTGCTGAGGAGAACCAAGTCAGTCTCCAGAGACTTCAACATCCCTG  
 GCTTCCCGACTGTGAGGTTCCTCAAGGCCCTTACCAAGAACGGCTCGGAGCAGTATTCCAGTGCTGGTGGTGC  
 ACGTGCAGACGCTGCGGGAGAGGCTCATTGACGCCCTGGAGTCCCATCATGACACGTGGCCCCAGGCTGTGCC  
 CACTGGAGCCTTGCCAAAGTGGAGGAGATTGATGGATTCTTGGCAGAAATAACGAGAGACTGCGGCTGTGATCT  
 TTGAAAAGGGAGGCTCCTACCTGGGTAGAGAGGTGGCTCTGGAGCTGTCCAGCACAAGGCGGTGGCGGTGGCGA  
 GGGTCTGAACACAGAGGCCAATGTGGTGAGAAAGTTGGTGTACCGACTTCCCTCTTGCTACCTGCTGTTCC  
 GGAATGGCTCTGTCTCCCGAGTCCCGCTGCTCATGGAAACAGGTCCTCTATACCGCTTACCTGCAGAGACTCT  
 CTGGGCTCACCAGGAGGCTGCCAGACACAGTTGCACCAACCACTGCTAACAAGTAGCTCCCCTGTTTGA  
 AATTGGCAGATCGCTCCAAGATCTACATGGCTGACCTGGAATCTGCACTGCATCATCTTGGGATAGAAGTGG  
 GCAGGTTCCCGGTCTCGGAGGGGAGCGCTGGTGGCTTGAAGATTTTGGCAGTGTGGCCAAAGTATTCC  
 CTGGCCGGCCCTTAGTCCAGAACTCTCTGCACTCGGTGAATGAATGGCTCAAGAGGCGAGAAGAAATAAATT  
 CCTACAGTTCTTAAAACTGCCCTGGACGACAGCAAGAGGGTGCCGTTCTTGCCAAAGAGGTGAATGATTG  
 ECTGCCAGGGAGTGAGCCGCAATTTCCGGGCTTTCCTGCTCCTGTGGGTCTCTTCCACTTCTTGACTGTGC  
 AGGCAGCTCGGCAAAATGTAGACCACTCAGGGAAGCAGCCAGGCGCAAGGAGGTCCTCCGAGCCTTCCGAGGCT  
 ACGTGCACACTACTTTCGGGTCCGAGACTGCGCTAGCCACTTCGAGCAGATGCTGCTGCTCCATGCAACCGG  
 TGGGGAGTCCCAAGCCGCTGTCTCTGTGCTGTAGCCACAACAGGGTCAATGCTGCGCTTGAGAGTGGCC  
 CCAGCGAGGACCCCAAGTTTCCCAAGGTGCACTGGCCACCCCTGAACTTTGTTCTGCTGCCACAATGAACGCC  
 TGGATGTGCCCGTGTGGGACGTGGGAAGCCACCTCAACTTCTCAAGGCCCACTTCTCCCAAGCAACATCATCC  
 TGGACTTCCCTGCACTGGGTGAGTGCCTGCCGAGGGATGTGCAGAATGTGGCAAGCCGCCCCAGAGCTGGCGATGG  
 GAGCCCTGGAGCTGGAAGCCGGAAATTAACCTCTGGAGCTGGGAAGCTGAGATGAGTGAAGTCCCCCACAACA  
 CCAACCCACATGTGCTCGGTGAGGAGCTCAGGCAAGTGGACCCCGAAGCTGACCTTGGCTCTCAGAGCTGCAC  
 CAGGCCAGAGCCTCTCTGAGCACATGGCAGAGCTTCAGAGGAATGAGCAGGAGCAGGCCCTTGGGAGTGGGACT  
 TGAGCAGCGGAGCACAGGGGCTGCATTGCTGGCTGAGTGCAGGCTGAGAAGAACCCGCTCTGGGGCCCTTTGG  
 AGGTGAGCGCGGTGGCGGCACTCCAGCAGCTGGTCGACATCCCTGAGGGCCAGGCTGGAGGCCCGAGCTGGAC  
 GGGGCCGAGGCCAGTGGCTGCAAGTGTCTGGGAGGGGGCTTCTCTTACCTGGACATCAGGCTCTGTGTGGGGCTCT  
 ATTCCCTGTCTTCTATGGGCTGCTGGCCATGTACACCTACTTCCAGGCCAAGATAAGGGCCCTGAAGGGCCATG  
 CTGGCCACCTGTGACGCT**TGA**ACCACTCTGGGAGGAGGCGGGAGAGGAGCTGCCATCTCTAGGCACCTCAAGCCC  
 CTTGACCCCATCTCCCTCCCTCCACCCCTTGTCTCTTGTCTGGCTAGAAGTGTGGGAAATTCAAGGAAAACGAG  
 TTGCTCCAGTGAAGCTTCTTGGGGTGTCTAGGACAGAGAGCTCCTTTCAGACAAAAGCAGGAGCAGGGTCCAGG  
 TCCCTCTGCTGTGCAAGGAGGGCAGCCCGGGCAGTGGGCATAGGGCAGCTCAGTCCCTGGCCCTCTTAGCACCCAC  
 ATTCTGTGTTTCAAGCTTATTGAAGTCTGCTCATCTTCACTGGAGCTCAGTCTCTCTCTCTTGGCTTGGC  
 CCTCAACTGGGCAAGTGAAGCAGGAGGCTCCCGCAGCTGGGTGGCTGGATGGAATGGAATCTCACTAGCTGC  
 TGGGCTCCGCGCACCTGCTCCTTCCGACAAATGAAGAAGCCTTTGCACCTGGGAGGAAGACCAACCCCGGG  
 CCCTCTATGCTCGGCGAGCTCCAGCTCCTCAGACACTCCTGGGTGGGCTTGGGCTTCAAGGTTGGGTTGTGAAGC  
 TTCTGGAAAGTGTGCTGGTCTCCAGGTGAGGCAAGCATGGTCTGGGCTGAGGAGTGAAGTGGCTGTGCTGTGT  
 GGGACTGACAGAGTGGTGGCATGGGAGGATGTGGGTCTCTAGTGCCTTGGCTGGCTTAGCTGAGGAGAGA  
 TGGCTGCTTCACTTCCCCCACTTGAGCTGCTGCTCCCTGAGCCTGGTCTTGTGCTCTTTTGTGCTCTC  
 CAGATGAATGCTCATCTTTGGAGGTTGCCAGTAGAAGCTAGGGAGGGAGTGTCTTCTCTCTCAGGTTTAC  
 CTTCAGTGTGCAAGATTAGAGGCTCTGGCGGGGCGAGTGCCTTACATGCTGTGATTCCCGCCCTACCCCT

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**FIGURE 212**

MRRNSGSGPPPSLLLLLLWLLAVPGANAAPRSALYSPSDPLTLLQADTVRGAVLGSRSAAVAV  
EFFASWCGHCIAFAPTWKALAEDVKAWRPALYLAALDCAEETNSAVCRDFNIPGFPTVRFFKA  
FTKNGSGAVFPVAGADVQTLRERLIDALESHDWTWPACPPLEPAKLEEIDGFFARNNEEYLA  
LIFEKGSYLGREVALDLSQHKGVAVRRVLNTEANVVRKFGVTDFFPCYLLFRNGSVSRVPVL  
MESRSFYTAYLQRLSGLTREAAQTTVAPTANKIAPTVMWKLADRSKIYMADLESALHYILRIE  
VGRFPVLEGQRLVALKKFVAVLAKYFPGRPVQNFHLHSVNEWLKRQKRNKIPYSFFKTALDDR  
KEGAVLAKKVNWIGCGQSEPHFRGFFPCSLWVLFHFLTQAAARQNVDHQSQAAKAKEVLPAIRG  
YVHYFFGCRDCASHFEQMAAASMRVGS PNAAVLWLWSSHNRVNARLAGAPSEDQFPKVQWP  
PRELCSACHNERLDVPVWDVEATLNFLKAHFSPSNIILDFPAAGSAARRDVQNVAAPPELAMG  
ALELESRNSTLDPGKPEMMKSPTNTTPHVPAGPEASRPPKLHPGLRAAPGQEPPEHMAELQR  
NEQEQLPGQWHLKSRDTGAALLAESRAEKNRLWGPLEVRRVGRSSKQLVDIPEGQLEARAGRG  
RGQWLQVLGGGFSYLDISLCVGLYLSFMGLLAMTYFQAKIRALKGHAGHPAA

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 705-728

**N-glycosylation sites.**

amino acids 130-134, 243-247, 575-579

**Glycosaminoglycan attachment site.**

amino acids 6-10

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 644-648

**N-myristoylation sites.**amino acids 52-58, 56-62, 196-202, 381-387, 392-398, 448-454,  
468-474, 684-690, 702-708**Cytochrome c family heme-binding site signature.**

amino acids 509-515

**Thioredoxin family proteins**

amino acids 62-78

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**FIGURE 213**

GCACGAGGCCGACTTCCAGACCATCTACAACCTGCACGGCCTGGAACAGCTTCGGCTCCGACAC  
TGAGATCATCCGGCTCAAGGAGCAAGGTTGCGAAATGAAGTCGGGAGCCGGGCTGGAAGCAGA  
GTCTGTGCCGATGCGCTCATCATTTGGGGTGGCCGTAGGAGCTGGTGTGGCCTTCCTCGTCCT  
TATGGCAACCATPCGTGGCGTTCTGCTGTGCCGTTCCAGAGAAATCTCAAAGTGTTGTGTGTC  
AGCCAAAAATGATATCCGAGTGGAATTTGTCCACAAGGAACAGCCTCTGGTCGGGAGGGTGA  
GGAGCACTCCACCATCAAGCAGCTGATGATGGACCGGGGTGAATTCAGCAAGACTCAGTCCT  
GAAACAGCTGGAGGTCCTCAAAGAGAGGAGAAAGAGTTTTCAGAACCTGAAGGACCCACCAA  
TGGCTACTACAGCGTCAACACCTTCAAAGAGCACCCTCAACCCCGACCATCTCCCTCTCCAG  
CTGCCAGCCGACCTGCGTCTGCGGGTAAGCAGCGTGTGCCACAGGCATGTCTTACCAA  
CATCTACAGCACCCTGAGCGGCCAGGGCCGCTCTACGACTACGGGCAGCGGTTTGTGCTGGG  
CATGGGAGCTCGTCCATCGAGCTTTGTGAGCGGGAGTTCCAGAGAGGCTCCCTCAGCGACAG  
CAGCTCCTTCTGGACACGAGTGTGACAGCAGCGTCAGCAGCAGCGGCAAGCAGGATGGCTA  
TGTGCAGTTTCGACAAGGCCAGCAAGGCTTCTGCTTCTCTCCACCCTCCAGTCCTCGTC  
CCAGAACTCTGACCCAGTCGACCCTGACGCGGCGGATGCAGACTCAGCTCTAAGGATCACA  
CACCGCGGGTGGGACGCGGCAGGGAAGAGGTGAGGCACGTTCTGGTTGTCCAGGGACGAGG  
GGTACTTTGACAGAGGACACCAGAATTGGCCACTTCCAGGACAGCCTCCAGCGCCTCTGCCAC  
TGCTTCTCTCGAAGCTCTGATCAAGCACAAATCTGGGTCCCCAGGTGCTGTGTGCCAGAGGT  
GGGCGGGTGGGAGACAGACAGAGGCTGCGGCTGAGTGCGCTGTGCTTAGTGCTGGACACCCG  
TGTCCCCGGCCCTTTCTGGAGGCCCTCTACCACCTGCTCTGCCACAGGCACAAGTGGCAG  
CTATAACTCTGCTTTCATGAAACTGCGGTCCACTCTCTGGTCTCTCTGTGGGCTCTACCCCTC  
ACTGACCACAAGCTCTACCTACCCCTGTGCTGTGCTCCCATACAGCCCTGGGAGAGGGGA  
TGACGTCTTCCAGCACTGAGCTGCCCCAGAAACCCGGCTCCCCACTGCTGCTCATAGCCCA  
TACCCTGGAGGCTGACAAGCCAGAAATGGCCTTGGCTAAAGGAGCCTCTCTCTACAGGCTG  
GCCGGGAGCCACCCCAATTGTTTGGTGTGTTTGTGTCCATACTCTTGCAGTTCTGTCTTG  
GACTTGATGCCGCTGAACTCTGCGGTGGGACCGGTCCCGTCAGAGCCTGGTGTACTGGGGGA  
GGGAGGGAGGAGGGAGCCTGTGCTGACGGAGCACCTCGCGGGTGTGCCCTCCTGGGCTGTG  
TGACCCAGCCTCCCCACCCACCTCCTGCTTTGTGTACTCTCCCTCCCCCTCAGCACAATC  
GGAGTTCATATAAGAAGTGCGGGAGCTTCTCTGGTCAGGGTCTCTGAACACTTATGGAGAGA  
GTGCTTCTGGGAAGTGTGGCGTTTGAAGGGCTGGAGGCGAGGTCTTTAAGATGGCGAGACT  
GCCCTTCTCAGCTGATAAACACAAGAACGGCGATCCTGTCTTCAGTAAGGCTCCACGAGAAGA  
GAGGAAGTATATCTACACCTCAACCCCTCTAGTCACCACCTGAAATAAATGTTAGGGAAAAAAA

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**FIGURE 214**

MAVIIGVAVGAGVAFVLVLMATIVAFCCARSQRNLKGVVSAKNDIRVEIVHKEPASGREGEEHS  
TIKQIMMDRGEFQQDSVLKQLEVLKEEEKEFQNLKDPTNGYYSVNTFKEHHSTPTISLSSCQP  
DLRFAGKQRVPTGMSFTNIYSTLSGQGRLYDYGQRFVLGMGSSSIELCEREFQRGSLSDSSSF  
LDTQCDSSVSSSGKQDGYVQFDKASKASASSSHHSQSSSQNSDPSRPLQRRMQTHV

**Signal peptide:**

amino acids 1-28

**Glycosaminoglycan attachment site.**

amino acids 150-154

**N-myristoylation sites.**

amino acids 6-12, 10-16, 36-42, 139-145, 165-171

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 114-125

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**FIGURE 215**

CAGCCTTCCTCCCCAGCCTGAGTGACTACTCTATTCCCTTGGTCCCTGCTATTGTCGGGGACG  
ATTGCAATGGGGTACGCCAGGAAAGTAGGCTGGGTGACCGCAGGCCTGGTGATTGGGGCTGGCG  
CCTGCTATTGCATTATAGACTGACTAGGGGAAGAAAACAGAACAAGGAAAAAATGGCTGAGG  
GTGGATCTGGGGATGTGGATGATGCTGGGGACTGTTCTGGGGCCAGGTATAATGACTGGTCTG  
ATGATGATGATGACAGCAATGAGAGCAAGAGTATAGTATGGTACCCACCTTGGGCTCGGATTG  
GGACTGAAGCTGGAACCAGAGCTAGGGCCAGGGCAAGGGCCAGGGCTACCCGGGCACGTCGGG  
CTGTCCAGAAACGGGCTTCCCCCAATTGAGATGATACCGTTTTGTCCCCCAAGAGCTACAAA  
AGGTTCTTTGCTTGGTTGAGATGTCTGAAAAGCCTTATATCTTGAAGCAGCTTTAATTGCTC  
TGGGTAACAATGCTGCTTATGCATTAAACAGAGATATTATTCGTGATCTGGGTGGTCTCCCAA  
TTGTGCGAAAGATTCTCAATACTCGGGATCCCATAGTTAAGGAAAAGGCTTTAATTGTCCTGA  
ATAAATTGAGTGTGAATGCTGAAAATCAGCGCAGGCTTAAAGTATACATGAATCAAGTGTGTG  
ATGACACAATCACTTCTCGCTTGAACATCATCTGTGCAGCTTGTGGACTGAGATTGCTTACAA  
ATATGACTGTTACTAATGAGTATCAGCACATGCTTGCTAATTCCATTTCTGACTTTTTTCGTT  
TATTTTCAGCGGGAATGAAGAAACCAAACTTCAGGTTCTGAAACTCCTTTGAATTTGGCTG  
AAAATCCAGCCATGACTAGGGAAGTGTCTCAGGGCCCAAGTACCATCTTCACTGGGCTCCCTCT  
TTAATAAGAAGGAGAACAAAGAAGTTATTCTTAAACTTCTGGTCATATTTGAGAACAPAAATG  
ATAATTTCAAATGGGAAGAAAATGAACCTACTCAGAATCAATTCGGTGAAGGTTCACTTTTTT  
TCTTTTTAAAAGAATTTCAAGTGTGTGCTGATAAGGTTCTGGGAATAGAAAGTCACCATGATT  
TTTTGGTGAAAGTAAAAGTTGAAAAATTCATGGCCAAACTTGCTGAACATATGTTCCCAAAGA  
GCCAGGAATTAACACCTTGATTTTGTAAATTTAGAAGCAACACACATTGTAACACTATTCATTTTC  
TCCACCTTGTTTATATGGTAAAGGAATCCTTTGAGCTGCCAGTTTTGAATAATGAATATCATA  
TTGTATCATCAATGCTGATATTTAACTGAGTTGGTCTTTAGGTTTAAAGATGGATAAATGAATA  
TCACTACTTGTTCTGAAAACATGTTTGTGCTTTTTATCTCGCTGCCTAGATTGAAATATTTT  
GCTATTTCTTCTGCATAAGTGACAGTGAACCAATTCATCATGAGTAAGCTCCCTTCTGTCATT  
TTCATTGATTTAATTTGTGTATCATCAATAAAATTGTATGTTAATGCTGGAAGA

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**FIGURE 216**

MGYARKVGWVTAGLVIGAGACYCIYRLTRGRKQNKEMAEGGSGDVDDAGDCSGARYNDWSDD  
DDDSNESKSIVWYPPWARIGTEAGTRARARARARATRRRAVQKRASPNSSDDTVLSPQELQKV  
LCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRD LGGLPIVAKILNTRDFIVKEKALIVLNN  
LSVNAENQRRLKVYMNQVCDTITSR LNSSVQLAGLRLLTNMTVTNEYQHMLANSISDFFRLF  
SAGNEETKLQVLKLLLNLAENPAMTRELLRAQVPSSLGSLFNKKENKEVILKLLVIFENINDN  
FKWEENEPTQNQFGEGLFFFLKEFQVCADKVLGIESHHDFLVKVKVGKFMAKLAEHMFPSQE

**Signal peptide:**

amino acids 1-20

**N-glycosylation sites.**

amino acids 68-72, 189-193, 217-221, 230-234

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-111

**N-myristoylation sites.**amino acids 13-19, 17-23, 19-25, 54-60, 83-89, 147-153, 255-261,  
290-296**Amidation site.**

amino acids 29-33

